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115913

From: Mehta, Ashwin
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CREF

STIC,

Please search the nucleotide sequences of SEQ ID NOs: 1-3 from 10/026,767.

My mail room is 2C18, office 2A19, art unit 1638.

Thank you,
Ashwin

Ashwin Mehta
United States Patent and Trademark Office
Biotechnology Patent Examiner
(571) 272-0803

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STIC

13 NA
1- 2549
2- 2571
3- 1833

3p

17 27

1- 137
3p 116
3h 115 22
4. 121.5
6p 110.5
6h 180

Searcher: O. Schreiber
Phone: 272-2526
Location: Ramsen E01A61
Date Picked Up: _____
Date Completed: 3/11
Searcher Prep/Review: 10
Clerical: _____
Online time: 6

TYPE OF SEARCH:
NA Sequences: 3
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: Compag
WWW/Internet: _____
Other (specify): _____

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

5
6
7
8
9
10
11
12

DATA9714 Cross section

AK102633 *Oryza sativa*

AK101985 Oryza sat

AK069425 *Oryza sativa*
M92286 *Actinidia chinensis*

AF067967 Mesembrya
AF0267 Solanum lyc

A.J.278818 Medicago

AB056452 Vigna unguiculata

Y09355 *A. thaliana*
AY091766 *Arabidops*

Accession	Sequence
I47781	Sequence 1
M92276	Vigna aconitifolia

AY080771 Arabidops

AY113046 Arabidopsis

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
D49714		Oryza sativa mRNA for delta1-pyrroline-5-carboxylate synthetase, complete cds.	D49714				
D49714.1		GI:2081611					
delta1-pyrroline-5-carboxylate synthetase; OSP5CS.							
Oryza sativa							
Oryza sativa							
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriartoideae; Oryzaceae; Oryza.							
22	1085.6	42.6	2185	8	AY113046		AY113046 Arabidops
23	1085.6	42.6	2185	8	AY150430		AY150430 Arabidops
24	1085.6	42.6	2552	8	ATP5CS3GN		X867737 A.thaliana
25	1085.6	42.6	2554	8	ATP5CS3MR		X97330 A.thaliana
26	1085.6	42.6	2630	8	AF444633		AF444633 Arabidops
27	1080.8	42.4	2571	8	ATP4TPPCS		D31218 Arabidops
28	1027.4	40.3	2603	8	MSP5CS1		X98421 M.sativa
29	416.6	16.3	1250	8	MSP5CS2		X98422 M.sativa
30	405.8	15.9	801	8	MTR478820		ABJ278820 Medicago
31	375.2	14.7	712	8	AB097403		AC111016 Arabidops
32	335.7	14.0	14605	8	AC111016		AC111016 Arabidops
33	342.2	13.4	3265	9	HSU868758		U68758 Human pyro
34	338.2	13.3	967	8	AF503911		AF503911 Sueda ma
35	336.2	13.2	3262	9	HSU6542		U76542 Human pyro
36	323	12.7	3442	10	AF056574		AF056574 Mus muscu
37	318.6	12.5	3435	10	BC037699		BC037699 Mus muscu
38	318.6	12.5	3472	10	BC033427		BC033427 Mus muscu
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40	314.6	12.3	2997	9	HSPECS		X94433 H.sapiens m
41	305.6	12.0	570	8	AF101444		AF101444 Cichorium
42	276.4	10.8	2903	3	AY069110		AY069110 Diosphill
43	265.4	10.4	452	8	AF022914		AF022914 Trilicium
44	245.4	9.6	11023	1	AE006391		AE006391 Lactococc
45	242	9.5	349082	1	EX572091		EX572091 Prochloro

TITLE Characterization of the gene for delta1-pyrroline-5-carboxylate and Shinozaki, K.

JOURNAL Plant Mol. Biol. 33 (5), 857-865 (1997)
MEDLINE 97260389

PUBMED	9106509
REFERENCE	2 (base)

2 (cases 1 to 2349)
Igarashi, Y., Yoshida, Y., Sanada, Y., Wada, K., Yamaguchi-Shinozaki, K.

TITLE Nucleotide sequence of a cDNA encoding and Shihozaki, K.

3 (bases 1 to 2549)
Yoshihisa Y.

QY 541 AAGTATACCAATATTTATGAAATGATGCCATCAGCACTAGAAGGCTCCATATAGG 600
 DB 541 AAGTATACCAATATTTATGAAATGATGCCATCAGCACTAGAAGGCTCCATATAGG 600
 QY 601 ATTCACTGCTGATATTCCTGGGATATGACAGTTTGACAGACTGTTGGCACTGAGTGA 660
 DB 601 ATTCACTGCTGATATTCCTGGGATATGACAGTTTGACAGACTGTTGGCACTGAGTGA 660
 QY 661 AAGCTATCTCTTATTCCTGCTCAGTATGATGAGTGGTGTATATAGTGTCCACCAAGTG 720
 DB 661 AAGCTATCTCTTATTCCTGCTCAGTATGATGAGTGGTGTATATAGTGTCCACCAAGTG 720
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 DB 721 AACCATCATCAAAAATCATACACACTTATATTAAGAAAGCAATCAGCAAGAAATCATCTT 780
 QY 781 TTGGAGCAAAATCTGCTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 840
 DB 781 TTGGAGCAAAATCTGCTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 840
 QY 841 TGGCTTCAAAATGAGGACACCTGCTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATG 900
 DB 841 TGGCTTCAAAATGAGGACACCTGCTGATGATGAGGATGAGGATGAGGATGAGGATGAGGATG 900
 QY 901 TTTAAGCTTCTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 960
 DB 901 TTTAAGCTTCTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 960
 QY 961 AATCATCTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 DB 961 AATCATCTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 QY 1021 ATCTACAGAAATTTGCTATCAAGAGGACGAAAGAAATGATGATGATGATGATGATGATGATGATG 1080
 DB 1021 ATCTACAGAAATTTGCTATCAAGAGGACGAAAGAAATGATGATGATGATGATGATGATGATGATG 1080
 QY 1081 TGGAGGCAAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
 DB 1081 TGGAGGCAAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
 QY 1141 TTGCTGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 DB 1141 TTGCTGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 QY 1201 GCTTGGCAAAATCTATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
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 DB 1801 TAAAGACAGAGAGATG 1860
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 QY 1921 ATGATGCTCAATCAGCAATG 1980
 DB 1921 ATGATGCTCAATCAGCAATG 1980
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 DB 2341 CTATATGCGGATG 2400
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 DB 2401 CAAAAATATATG 2460
 QY 2461 AAGTAAATCAGATG 2520
 DB 2461 AAGTAAATCAGATG 2520
 QY 2521 ACTAACATGCTGATG 2580
 DB 2521 ACTAACATGCTGATG 2580

RESULT 4
 AK101985
 LOCUS
 DEFINITION
 Oryza sativa (Japonica cultivar-group) mRNA linear PLN 24-JUL-2003
 Insert sequence.
 ACCESSION
 AK101985
 VERSION
 AK101985.1 GI:32987194
 KEYWORDS
 FLI CDNA; CAP trapper.
 SOURCE
 Oryza sativa (Japonica cultivar-group)

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriocarideae; Oryzoideae; Oryza.

REFERENCE
1
The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotte, I.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Ohtsuki, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tanoda, Y.,
Narikawa, R., Sugiyama, A., Mizuno, K., Kobayashi, M., Xie, Q., Lu, M.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Komono, H., Miyazaki, A., Oeato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
22752273
12869764

TITLE
2 (bases 1 to 1821)
Adechi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,
Hori, F., Hotte, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kawagashira, S., Kato, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Komono, H., Kouda, M.,
Koya, S., Kurihara, C., Kurose, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Nanaki, T., Narikawa, R., Nishikawa, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohtsuki, S., Ohtsuki, K., Oka, M., Ooka, H.,
Oeato, N., Ota, Y., Ohtsuki, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, T., Tagami, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, S., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yabuchi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and
Yoshimura, A.

REFERENCE
JOURNAL
MEDLINE
PUBMED
AUTHORS
TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:kikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
NIRS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotte, I., Kojima, K., Nanaki, T.,
Ohtsuki, E., Yabuchi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and
Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurose, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Nishikawa, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tanoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,

Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kawagashira, S., Kato, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Komono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohtsuki, S.,
Oka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami, T., Tanaka, S., Tomaru, A., Toya, T., Waki, K.,
Takaku-Akahira, S., Tanaka, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A., and Hayashizaki, Y.

FEATURES
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1.1821
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/mol_type="mRNA"
/cultivar="Hidponbare"
/db_xref="taxon:39947"
/clone="U033078N24"

ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1798; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GCGGCTGCGCGCGCAAGCGCGAGACGTGGAGAGGATTTACAGTAGAGGAGAGG 60
21 GCGGCTGCGCGCGCAAGCGCGAGACGTGGAGAGGATTTACAGTAGAGGAGAGG 80
61 TGGAGAGAGAGAGGCGTGGAGCGTGGAGAGCGGTTGCGCATGGCGGCGGCGGCGC 120
81 TGGAGAGAGAGAGGCGTGGAGCGTGGAGAGCGGTTGCGCATGGCGGCGGCGGCGC 140
121 GGAGCTTGGTGGAGAGCGTGGAGCGGCGTGGAGAGCGGTTGCGCATGGCGGCGGCGC 180
141 GGAGCTTGGTGGAGAGCGTGGAGCGGCGTGGAGAGCGGTTGCGCATGGCGGCGGCGC 200
181 GCAAGAGAGAGAGGATTTGGCTTGGCGAGGTTGGAGCGTGGAGAGCGGTTGGAGAG 240
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361 TGAAGTATGAGTGAAGAGGCTTGGCGGCTTGGCTGAGAGTGAAGTGAAGTGAAGTGAAG 420
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421 ATATGTTGTTTAAACCACTGAGATGCTGCTGATCTCACTTCTTGTCCACCAAGTGAAT 480
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501 TTGAAGACCAAGATTTGGCGGAGCACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 560
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561 AAGTTATACCAATATTTATGAAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 620
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681 AAGTGAATCTCTTATTTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 740
721 AACCATATCAAAATATATACACTTATTTAAAGAAAGCAATGCAAGAAATCACTT 780

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Db	801	TTGGAGACAATCTCGTGTAGGTATAGAGAGGATATACAGCAAAATGAAAGCTGTGTCT	860
OY	841	TGCGTTCAAAATAGCGGACACCTGTGTATATCAAGTGGGTTGMAAATCGAGCATTC	900
Db	861	TGCGTTCAAAATAGCGGACACCTGTGTATTTACAAGTGGGTTGMAAATCGAGCATTC	920
OY	901	TTAAAGTCTTCAATGGGGAAAAAATTGGTACTCTTTTCACAAGATCGCAATTTGTGGG	960
Db	921	TTAAAGTCTTCAATGGGGAAAAAATTGGTACTCTTTTCACAAGATCGCAATTTGTGGG	980
OY	961	AATCATCTAAGATATTGTACTCGTGAATAGGCTGTGGCGCAAGATGTTCAAGGC	1020
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OY	1021	ATCTACAGAAATTTGTCATCAAGAGAACAAAAAGATATTTGCTAGATGTTCAGATGCTT	1080
Db	1041	ATCTACAGAAATTTGTCATCAAGAGAACAAAAAGATATTTGCTAGATGTTCAGATGCTT	1100
OY	1081	TGGAGGCAATAGAGGATTTAATAGCTGTGAATGAAGATGATAGTACTCGCGCCCAAG	1140
Db	1101	TGGAGGCAATAGAGGATTTAATAGCTGTGAATGAAGATGATAGTACTCGCGCCCAAG	1160
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OY	1261	AAAAGACAGAGGTTGCTGATGATTTAGTCTTGAGAAACATCTTGCCATTAGGTGTTG	1320
Db	1281	AAAAGACAGAGGTTGCTGATGATTTAGTCTTGAGAAACATCTTGCCATTAGGTGTTG	1340
OY	1321	TCTTAATTTGTTTGGAGTCCCGACCTGATGCCCTTGTTCAATTTGCATCTTTGGCAATTC	1380
Db	1341	TCTTAATTTGTTTGGAGTCCCGACCTGATGCCCTTGTTCAATTTGCATCTTTGGCAATTC	1400
OY	1381	GAAAGGTAAATGTCCTTCTCTAAAGGTGAAAGAAAGCTATCAGATCAACAACGATAT	1440
Db	1401	GAAAGGTAAATGTCCTTCTCTAAAGGTGAAAGAAAGCTATCAGATCAACAACGATAT	1460
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Db	1821	T 1821	

[illegible]

Yamamoto, M.
 FAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Masuda, H., Mitsu, J.,
 Munro, K., Nariikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S.,
 Sushiyama, A., Suzuki, Y., Tsumoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Science Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hangaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiwamoto, K.,
 Hirotsu, T., Hori, F., Iida, J., Imamura, K., Imoto, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
 Kishikawa-Hirozane, T., Kojima, Y., Konno, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Otsu, N.,
 Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
 Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagami, T., Tagami, Y., Tagawa, A., Takahashi, F.,
 Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
 Yasunishi, A. and Hayashizaki, Y.

FEATURES

source

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 ORGANISM Oryza sativa (japonica cultivar-group)
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 REFERENCE 1
 AUTHORS The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team:
 Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Oono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurokawa, T., Kodama, T., Masuda, H., Kobayashi, K., Xie, Q., Lu, M., Marikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kaga, I., Kondo, S., Kono, H., Miyazaki, A., Oosato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shitaki, T., Yoshino, M., and Hayashizaki, Y.
 TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice.
 JOURNAL Science 301 (5631), 376-379 (2003)
 MEDLINE 22752273
 PUBMED 12869764

REFERENCE

2 (bases 1 to 3386)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiyama, K., Hiyama, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kaga, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kondo, M., Koyas, S., Kuribara, C., Kurokawa, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Mura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nakikawa, R., Nishikawa, J., Nishi, K., Nomura, K., Numaeki, R., Ohneda, E., Ohtsuki, K., Oka, M., Ooka, H., Oosato, N., Ota, Y., Oono, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Sato, K., Shibata, K., Shingawa, A., Shitaki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, N., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S., and Yoshimura, A.

TITLE

JOURNAL

Submitted (05-DEC-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT

This clone is one of the 28k full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project team: Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

PALS Genome Sequencing & Analysis Group: Oono, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurokawa, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J., Mizuno, K., Nishikawa, R., Nishikawa, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiyama, K., Hiyama, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kaga, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Kono, H., Konda, M., Koyas, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Mura, M., Nakamura, M., Nishi, K., Nomura, K., Numaeki, R., Oono, M., Oosato, N., Ota, Y., Saitoh, H., Sasaki, D., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shitaki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

FEATURES

source

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Best Local Similarity 54.1%; Score 1379; DB 8; Length 3386; Matches 1673; Conservative 0; Mismatches 490; Indels 0; Gaps 0;

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 AUTHORS Walton, E.F., Podivinsky, E., Wu, R.-M., Reynolds, P.H.S. and
 Young, L.W.
 TITLE Regulation of proline biosynthesis in kiwifruit buds with and
 without hydrogen cyanamide treatment
 JOURNAL Physiol. Plantarum 102, 171-178 (1998)
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 AUTHORS Walton, E.F., Podivinsky, E., Wu, R.-M., Reynolds, P.H.S. and
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 247 TTGCTATCTGCAAAAGCCACAAATTGAATGATGGAAGGCAATGTGCACTGTGGGC 306

Qy 397 AGGTGACCTGATGCGCTCTTTAGCATATGTTGTTTACCAACTGATGTCCTCATCTC 456
 Db 307 AAATGTCATTATGGCTCTTATGATACATTTGTTTGTAGCTGAGTGGATCATGCTC 366
 Qy 457 AACTTCTTGCACCGACAGATTTTGAACCCAAAGTTCGGGAGCAACTCACTGAA 516
 Db 367 AGCTACCTGTTACTGATTAATGATTTAGGATCCAAATTCAGGAAGCAACTTACTGAA 426
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 Db 487 GCACAGGAAGTCTCATATGAGAGCGCTTCTGTATATTTCTGGATTAATGACAGTTGAG 546
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 Qy 757 AAAAGCATCAGCAAGAAATCACTTTTGAGACAAATCTGTGATGATAGAGAGCATGA 816
 Db 667 AAATGTTGAGGAGCTGATTAATCTTTTGGGACAAATCCAGGGTGGAGAGGGGGCATGA 726
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 Qy 1417 AAGCTATCAGATCAACAGATATTCATTAAGTTTAACTGATGATTTCTCTGATG 1476
 Db 1327 AAGCTAATAATCTTAATGCAATCTTGCAGAGTTATTAATCTGCAATCTCTGAAATG 1386

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QY	1954	GTTATGGAAGTCTCATACAGATTTGTATTCGTCACATCAATGATTAAGGTAGCAGACTT	20133
Db	1899	AGCATGGAAGTGCCACACCGATACATCATTAATCGAAGATCAGAAATTTCTGAAGTTT	19588
QY	2014	TTCTACGACAGATTGATAGTGTGCTGTATTTCAATATGCAAGTACGAGATTTCTGTATG	20733
Db	1959	TTTATCGTACAGTTGACAGTGTCTGTATTTTCAACAGCAAGTACAAGATTTTATGTATG	20188
QY	2074	GAGCTCGTTTGGATTTGGGTGTAGTGTGGCATTAAGACACAGGGGTATTCATGCGCTG	21333
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QY	2134	GACCAAGTGGTGTGTAAGTCTCTTAACTTAACACATGATCTTTCGAGACGTGGCGAAG	21933
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QY	2234	TGTGTAATGATGACAAAGATGTCTGTATCAACCCATAAAGTCTTCTTTGGAAG	2248
Db	2139	TTGTTGATGATGATTAATCAATTGTGTATGTCACAAAGACCTTACTGACAAAG	2193

RESULT 10	
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DEFINITION	Vitis vinifera mRNA for pyrolysine-5-carboxylate synthetase (delta 1

[illegible]

	ORIGIN	
Query Match	44.9%	Score 1143.6; DB 8;
Best Local Similarity	71.4% ^a	Pred. No. 4,6e-274;
Matches 1536;	Conservative	0; Mismatches 609;
		Indels 7; Gaps 2

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Qy	878	TGGGTTTGAANAATCGAGCAATCTTAAAGTCTTCAATGGGGAAAAATTGGTACTCTT	937
Db	833	TGGGATCTCTCTGAAAGTATCTTAAAGTCTTATGGGGCGGTATTGGCACTCTT	892
Qy	938	TCACAAGATGCGAATTTTGGGGAATCACTAAGATGTATGACTCGTGAGATGGCTGT	997
Db	893	TCATGGAATGECTTATTAATGGGTCAAGTTAAAGATGGCGACGTGAATGGCAGT	952
Qy	998	TGCGCAAGAATTTGTCAAGGCATCTACAGAATTTGTATCAGAGAACGAAAAAGAT	1057
Db	953	TGCAGCAAGGAAAGTTCCAGGCGGCTTCAGGCAATGCTTCAACAAGACAGGAAGAAAT	1012
Qy	1058	ATTGTGATGTGTGAGATGCTTTGGAGCAATATGATTTTAATAGTCTGAATAAG	1111
Db	1013	TTTACTGACATAGCAATGCACTGGAACCAATAGAAGCTGATTAATAATTTGAAATGA	1072
Qy	1118	AGCTGATGTAGCTGGGCGCAAGTTGCTGATATAGAAGCTTGTGTGTAGATTGAC	1177
Db	1073	TGCTGATGTGAGGACACAACTGGCTGGAATGAAAAATCATTTGTTTCAAGCTGGT	1133
Qy	1178	TATTAACCAAGAAAGATAGCAAGCTTGCATAATCTTATGTTACCTTGCATAATGGA	1233
Db	1133	CTTAAGGCTGGAAGATTTCAAGGCTTGCAAACTCAATCTGTGCTTGCAAACTGGA	1192
Qy	1238	AGACCCCTATTAACCGAGTACTTAAANAAGACAGAGTGTGTGATTTAGTTAGTCTTGAGA	1297
Db	1193	AAGACCAATTTGGTCAATGTTTGAAGAAAACTGAAATTTGCAGATGSACTTACTTGAAAA	1255
Qy	1298	AACATCTTGCCCATTAAGTGTCTCTTAATGTTTGAATCCGAGCTGATGCTTGGT	1357
Db	1253	GATGTCATGCCCATTAAGGTGTGCTCTTAATGTTTGAATCTGACCAAAATGCTCTGGT	1312
Qy	1358	TCAGATTCACTCTTGGCAATTGCAAGGTGAATGCTCTCTCCATAAAGGGAAGAAAG	1412
Db	1313	ACAGATAGCTCATTAGCAATCCGAGGTGGGATGSACTTCTTGAAAGGTGAAAAAG	1372
Qy	1418	AGCTATCAGATCAAAACAGATATATGATTAAGTTTAACTGATGCTATTCCTGTATGT	1477
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Qy	1478	TGTGTAANAACCTAATTTGGCCTTGTTAACAATAAGATATGAGATTTGCTTAAGCT	1533
Db	1433	TGGGAAAGGCTAATTTGACCTTGTACTTCAAGAGGAGATCCCTAATCTCTCAAGCT	1493
Qy	1538	TGATGATGCTATGATCTTGTCACTCCAAAGAGATATAAGTGTCTCTCAATCAA	1597
Db	1493	TGATGATGTGATCGACCTTGTATATCCAAAGGACGACATTAACCTGTTTCTCAATAAA	1555
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Qy	1658	CAAACTCAGCTGCATGATATGGAATGGCAAACTTAATTTATGATGTCAAAAACGATTAACC	1712
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Db	1673	TGCAGCTGTATGCAATGAGAAACCTTCTGTATACAAAGGTTTATGCGACACTGTGG	1733
Qy	1778	CGTTGACGACATTAATAGACACTAANAACGANAAGACTTAATTTATGGGAGCCAT	1833
Db	1733	CTTCAATAGCTTATGTAAGCTCCGCAATGAAGGGGTACTTATATATGGTGAACAA	1792
Qy	1838	TGCGCAAAAGCTCTGGGATTTCCAAAAGCTGTTTCATTTCACTATGAGTATAGTCTAT	1897
Db	1793	GGAAGTCTCTGCGAATCTTCCAGAGCTCACTCTTTCATCATGAGTAAATTCAT	1855
Qy	1898	GGCTTCGACTGTGATTTGTTGAATGATGTTCAATCAGCAATGACCAATATTCATCTGTTA	1955
Db	1853	GGCTTCGACTGTGATTTGTTGAATGATGTAATTTCCATGTATCATATTCACCGCA	1912

ORIGIN

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Query Match 44.6%; Score 1137.4; DB 8; Length 2520;
 Best Local Similarity 70.9%; Pred. No. 1.6e-272;
 Matches 1510; Conservative 0; Mismatches 621; Indels 0; Gaps 0;

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 71 ATGGCAGCGCGAGCCCTTGTAGATTTCGTCAAGATGTTAAAGCATATCATCAAG 130
 159 GTGGGACATGCAATGTTCTCCAGACAAATGGAATGGCTTGGGAGGGTTGAGCT 218
 131 GTTGGTACTGCTGTGTATCTGCCAAGATGGAATGAGCTTGAAGAAATTAAGGGGCA 190
 219 CTGTGCGAGCAGATTAAAGAACTGAATCTTTAGAGTAAAGATGTTGGTCACTCA 278
 191 CTCTGAGCAGATTAAGAGGCTTAACATCTTGGTATGAAGTATTTAGTTTCAATCA 250
 279 GGTGCTTTGAGTGGGCGCAGACGACTTGAATACCGAAGCTTGTCAATAGCACTTT 338
 251 GGTGCTTTGAGTGGTGGTCCCAAGGCTTGAATTAAGAAATGATCAAGATGTTT 310
 339 GGTGATCTGCAGAAAGCAGACAGATGAGTGAATGAAGAGCTTGGCGCTTGGTGCAG 398
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 1539 GAT 1598
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 1599 GCGTCAACTAAGATCTGTTCTTGGGCAATGCTGATGATGATGATGATGATGATGATGATGAT 1658
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 1899 GCGTCACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1958
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 1959 GGAAGTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2018
 1931 GGAAGTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1990
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Qy      1669  ACATGATATGCAAAACTTATTTGATGATGCAAAACTGATTAACCAAGCTGCA 1728
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Db      1813  TTATATAGCCCTGCAAGCAATGATGCTCACTTTGATGATGAGGCAAAAGCA 1872
Qy      1849  CTTGAGATTTCCAAAGCTGTTTATTTATCATGATGATGATGATGATGATG 1908
Db      1873  AACTGATATTCGGAAGTAAATATTTATTTATTTATTTATTTATTTATTTAT 1932
Qy      1909  TTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1968
Db      1933  TTGAATTTGTAAGAACCTGACACGCTGCTATGATGATGATGATGATGATG 1992
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Qy      2149  AAGCTCTCTTAATCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2208
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RESULT 13
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 ACCESSION AB056452
 VERSION AB056452.2 GI:37951331
 KEYWORDS
 SOURCE Vigna unguiculata (cowpea)
 ORGANISM Vigna unguiculata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Vigna.
 1
 Iuchi, S.
 Drought inducible gene from cowpea
 JOURNAL
 Unpublished
 2 (bases 1 to 2791)
 Iuchi, S.
 Direct Submission
 Submitted (26-FEB-2001) Satoshi Iuchi, RIKEN, Plant Molecular
 Biology, Kouyadai 3-1-1, Tsukuba, Ibaraki 305-0074, Japan
 (E-mail: iuchi@rtc.riken.go.jp, Tel:81-298-36-4359,
 Fax:81-298-36-9060)
 On Oct 24, 2003 this sequence version replaced gi:13161404.
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ORIGIN

Query Match 43.8%; Score 1115.6; DB 8; Length 2791;
 Best Local Similarity 70.1%; Pred. No. 4,5e-267;
 Matches 1499; Conservative 0; Mismatches 639; Indels 0; Gaps 0;

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Qy      229  AGGTTAAGAACTGAACCTTTAGATAGAAATTTTGGTACCCTCAGGTGCTG 288
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Qy      289  GAGTGGGAGCAGAGCACTTAAAGTACCGGAAGCTTGTCAATAGCAAGCTTGT 348
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 Db 956 CAACAAATATCAACGGGTTCTTCAAGGGAAAAAGATAGTACTGCTTCAATAAGATG 1015
 Qy 949 CGAATTTGTTGGGATCATTAAGATTTAGATCTCTGATAGATGCTGTTGGCGAAG 1008
 Db 1016 CTCACTTTGGGACCAATATTAAGAAAGAGAGTCAAGTAAATGGCAATTTGACAGCGG 1075
 Qy 1009 ATTTGCAAGGCACTTACAGAAATTTCTCATGAGGAAAGAAAGAAATATGCTAAGATG 1068
 Db 1076 AGAGTTCTAAGAGATCTCAGATCTCAAACTGAAAGAAAGAGTAAATATTAATGGCAA 1135
 Qy 1069 TTGCAAGATGTTTGAAGGCAAAATGAGATTTAATAGTCTGAGATGAGAGCTGATGAG 1128
 Db 1136 TTGCTGATGATTTGAGAAAATGCAAGTGCATATGCTTGAATGAGAGTGAATGTTG 1195
 Qy 1129 CTGCGGCCCCAAGTGTGCTGATATGAGAGCTTTGTTGCTGATGATGATATATAAACCAG 1188
 Db 1196 CTGATCTGTGCTGCTGATATGAAATTTCTGATATCAGCTTAAACCTGAAACATG 1255
 Qy 1189 GAAAGATAGCAAGCTTGCAAAATCTATTCTATCCCTTGCAAAATAGGAAAGCCATATA 1248
 Db 1256 AGAAGATCTTAAGCTTGCAAAATCTGTGCGCATTTGGCAGCTATGAAAGAACCAATTTG 1315
 Qy 1249 ACCAGATCTTAAAGAAAGACAGAGTGTGATGATTTAGTCTTGAAGAAACATCTTGGC 1308
 Db 1316 GTCAAAATTTTAAAGAAAGACAGATGAGATTAATCTCCTGAGAAATTTATGATG 1375
 Qy 1309 CATTAGGATGTTCTTAAATGTTTTGAGGCCGAGCTGATGCTGCTGATGATGAT 1368
 Db 1376 CTTTGGAGCTCTTCTGTTATTTGAGATCTGACCAATGCCCTTGTGCGAATAGCTG 1435
 Qy 1369 CTTTGGCAATGGAAGTGTATGTTCTCTCTTAAAGGTGAAAAGAGATTAATCAAT 1428
 Db 1436 CATTGGCAATTCGAATGGGAATGTTTACTGCTTAAAGGTGAAAAGAGCCCAAGAT 1495
 Qy 1429 CAATACGATATGCAATAGGTTATTAAGTATGATGCTTCTGCTGATATGTTGTTGAAAAC 1488
 Db 1496 CAATATCAATCTTACACAGGTCATTAATCTGCTGATTCCTGATGCTGATGCTGATG 1555
 Qy 1489 TTAATGGCTTTGTAACAATGAGATGAGATGCAAGATTTGCTTAAAGCTTGAATGCTCA 1548
 Db 1556 TTAATGGCTTTGTAACAATGAGATGAGATTCATACCTAATTAAGCTTGAATGCTCA 1615
 Qy 1549 TTAATCTTGTCACTCAAGAGGAAATTAAGTGTCTCTCAATCAAGGCTGCACTA 1608

Db 1616 TAGATCTTGTGTTCCCAAGGACATATTAATCTGTTTCTCAATACAGAGCTCAACA 1675
 Qy 1609 AGATTCCTGTTCTTGGGCAATGCTGATGATATATGCAAGTATATATGACAAATCAGCTG 1668
 Db 1676 AAATTCCTGTTCTTGGGCAATGCTGATGATATATGCAAGTATATATGCAAGTATGCTA 1735
 Qy 1669 ACATGATATGCAAACTTATGTAATGATGCAAAAATGATTTACCGAGGCTGCA 1728
 Db 1736 AGATTTGATGCAAAACATATTTTGAAGATGCAAAAGATGATTTCTCGAGCTGCA 1795
 Qy 1729 ATGCAATGAGACCTTATCTAATGATGATGATGATGATGATGATGATGATGATGATG 1788
 Db 1796 ATGCAATGAGAACTCTTCTGATCAAGAGATCTATCAAAATGATGATGATGATGATG 1855
 Qy 1789 TATAGTATGACCTTAAACAGAGGCTTAAATTTATATGATGATGATGATGATGATG 1848
 Db 1856 TTGCTGTAATCTCAACGTGAAGGTTTAACTGATGATGATGATGATGATGATGATG 1915
 Qy 1849 CTCTGGATTTCCAAAAGCTGTTTCAATTCATGATGATGATGATGATGATGATGATG 1908
 Db 1916 TACTAAATATGTTGAACAAGGCTTTTCAATGATGATGATGATGATGATGATGATG 1975
 Qy 1909 TTGATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1968
 Db 1976 TTGAATTTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2035
 Qy 1969 ATACAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2028
 Db 2036 ATACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2095
 Qy 2029 ATAGTCTGCTGATTTCTAATGCAAGATGATGATGATGATGATGATGATGATGATG 2088
 Db 2096 ACAGTCTGCAAGTTTCCAAATGCAAGTCAAGATTTGATGATGATGATGATGATG 2155
 Qy 2089 TGGTGTGATGATTTGCAATAGCAAGGCTGATGATGATGATGATGATGATGATG 2148
 Db 2156 TTGATGCAAGGTTGCAATAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2215
 Qy 2149 AAGTCTCTTAACTACAGATGATGATGATGATGATGATGATGATGATGATGATG 2208
 Db 2216 AGGTTTATTAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 2275
 Qy 2209 AGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2246
 Db 2276 AAGAAATCAATTAACGTAAGAGATTTGCACTAGAA 2313

RESULT 14
 AF314811
 LOCUS 2551 bp mRNA linear PLN 06-FEB-2001
 DEFINITION Brassica napus delta 1-pyrroline-5-carboxylate synthetase A mRNA,
 complete cds.
 ACCESSION AF314811
 VERSION AF314811.1 GI:12667248
 KEYWORDS
 SOURCE
 ORGANISM
 Brassica napus (rape)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 2551).
 Kang Y.H. and Lee S.Y.
 Isolation of a gene encoding the delta 1-pyrroline-5-carboxylate
 synthetase A in Brassica napus
 Unpublished
 2 (bases 1 to 2551)
 Kang Y.H. and Lee S.Y.
 Direct Submission
 Submitted (19-OCT-2000) Lab. of Biochemistry, Graduate School of
 Biotechnology, 1, 5-ka, Anam-dong, Sungbuk-ku, Seoul 136-701,
 Rep. of Korea
 FEATURES
 Location/Qualifiers
 1..2551

QY 877 GTGGATTGAAAAATCGAGCATCTTAAAGTCTTACGAGGAAAAAATTGACTCTCT 936
 Db 853 GTGATATGCAAGTGAATAATAGTAAAGTCTTAAAGACTCGCGTTGGTACCTCT 912
 QY 937 TTCAAGAAATGCCAATTTTGTGGGAATCATCTAAAGATGTTAATTAATCTCGGAATAGGCTG 996
 Db 913 TCCATCAAGATGCTCAATTTATGAGGCTCCGCTCGTAGTACTCTTCGTAACATGACG 972
 QY 997 TTGCGCAAGAGATTTGTTCAAGGATCTAAGATTTGTCATGAGAGAAAAAGA 1056
 Db 973 TTGTCGCAAGGAGAAAGCTCAAGAAAGCTTCAGGCTTATCTTCAAGAAATAGAAAAA 1032
 QY 1057 TATTGCTAGATGTTGTCAGATGCTTTGAGGCAATGAGATTTAATTAAGCTTGAAGATG 1116
 Db 1033 TTCTACACGACATGTCCTAAGCTTGAAGTAAATGAGAAAAAATTTAAAGCTGACAAATG 1092
 QY 1117 AAGCTGATGTAGTGTGCGGCCCAAGTTCTGGAATATGAGAGCTTTGTTGCTAGATTGA 1176
 Db 1093 ATTGATGATGTTGTCGACACACAGACATGATATGAGAGCTCTTGTAGCTCGCTTAG 1152
 QY 1177 CTATPAAACAGAAAGATAGCAAGCTTGCAGAAATATTTCTGACCTTGCAGAAATG 1236
 Db 1153 TTATGAAAGCTGGAAGATCTCAAGCTTGCAGCTTCCGTTCCGACGCTAGCCGAATG 1212
 QY 1237 AAGACCTATPAAACAGATCTTAAAGACAGAGCTTGCATGATTTAGTTCTTGAGA 1296
 Db 1213 AAGATCCATAGGCGCGTATTTAAAGAAATCTCAGTTGACAGATGATCTTATTTAGAGA 1272
 QY 1297 AAGATCTTGCCCATTAAGTGTCTTAAATGTTTGAAGTCCGACCTGATGCTTGG 1356
 Db 1273 AGACCTCATCAACATAGTGTCTTCTGATGTTTGAATCCGCGCTGATGCACTTG 1332
 QY 1357 TTGATTTGATCTTTGGCAATGGAAGTGTAATGCTCTTCTPAAAGTGGAAG 1416
 Db 1333 TTCAATAGCTTCCCTTGCAATCCGAGTGGAATGCTTCTGCTGAGAGGGAAG 1392
 QY 1417 AAGCTATCAGATCAACACAGATATGATAGATTAATTAATGCTATTCCTGTAATG 1476
 Db 1393 AGGCTCGATCAATGCTATCTTACACAGGATGATCACTGATGCAATCCGAGACTG 1452
 QY 1477 TTGCTGAAAACTTATGAGCTTGTTCACACTAGAGATGAGATGCGAGATTTGCTAAAG 1536
 Db 1453 TTGAGGTAACCTATGAGACTGTGACTTCAAGAGAGATTCCTGATTTGCTCAAGC 1512
 QY 1537 TTGATGATGTCATGATCTTGTCACTCCAGAGAGATTAATTAAGCTTGTCTCAATCA 1596
 Db 1513 TTGATGAGCTTATGATCTTGTGATCCAGAGAGGCAACAAGCTTGTCTCAATTA 1572
 QY 1597 AGGCTCACTAAGATTCCTGTTCTTGGGCACTGATGATATGCGCAGTATATG 1656
 Db 1573 AAAACTCGACGAAAAATCCAGTGTAGCCCATGCTGATGATCTGCAATGATATGTTG 1632
 QY 1657 ACAATCAGTCACTGATGATGCAAACTTATTTGATGATGCAAAACTGATTAAC 1716
 Db 1633 ATTAAGTCTGATTAAGTCACTGACATGCAAAAGGCAATGTTCCGATGCAAAAGTGAATAC 1692
 QY 1717 CAGCAGCTGCAATGCAATGAGACCTTACTAGTTCAATTAAGATCTTATGAAGTCCAG 1776
 Db 1693 CAGCAGCTGTAATGCGATGAAAACTTCTTGTACATTAAGATTTGAGCAGAAATGTT 1752
 QY 1777 GCCTTGAAGACATTTATAGTACATTAAGAAAGAGATTAATTAATTAATGATGAGCTTA 1836
 Db 1753 TTCTGATGATCTTATTTATGTTCTGCAACCAAGGCTGCACTTGTATGCTGGGCAA 1812
 QY 1837 TTGCGCAAAAGCTGCGAATTTCCAAAAGCTGTTCAATTTCAATGATAGTATGTTCTA 1896
 Db 1813 GAGCAAGTCAAAATCTGAATATCCGGAACAAATATCAATTCACAGATGACGTTCCA 1872
 QY 1897 TGGCTGCACTGTTGATGTTTGAATGATGTTCAATGCAAAATGACCATTAATCATGTT 1956
 Db 1873 AGGCTGCACTGTTGAATTTGTAAGAGCTATATGATGCTATGATCATATTCACCAAC 1932

QY 1957 ATGGAAGTCTCATACAGATTTGATTCCTCACTACATAGATGATAGGTTGCAAGACTTTTC 2016
 Db 1933 ATGGAAGTCAACACATGATTTGATGATGACGGAAGATGAGTGAAGTGAAGAAATATTC 1992
 QY 2017 TAAGCAGAGTTGATGATGCTGCTGATTTGATTAATGCAAGTACAGATTTCTGATGAGG 2076
 Db 1993 TCCGCAAGTGAACAGTCTGCTGTTTCCAAATGCAAGACAAAGTTCTGATGTT 2052
 QY 2077 CTGCTTTGATGATGAGTGTGAGGTTGAGGATGACACAGGCGTATCCATGCCCTGAC 2136
 Db 2053 TTAGCTTGAAGCTTGTGCTGATGAGTGGGATPACACAGCAGGATTCATGCCCTGATC 2112
 QY 2137 CAGTGGGTTGAAAGTCTCTTAATCTACAGATGATCTTCCAGAGACGTTGGGCAAGTGG 2196
 Db 2113 CAGTTGAGTTGAAAGATTTATGACACAGATGATTAATGAGAGAAAGGAAAGATG 2172
 QY 2197 TGAATGATGACAGAGATGCTGTGACACCAATPAAAGTCTTCTT 2242
 Db 2173 TGATGAGACATGAAATCGTTTACACCCATPAAAGATCTTCTGT 2218

Search completed: March 10, 2004, 19:21:58
 Job time : 9582.21 secs

XX The invention relates to a grass plant in which a delta¹-pyrroline-5-carboxylate synthase (P5CS) gene of rice, or a P5CS gene of Arabidopsis thaliana and the antisense gene of a proline dehydrogenase (ProDH) gene of Arabidopsis thaliana, have been introduced in tandemly connected relation to each other. A new method of the present invention is useful for the production of a transgenic rice plant with improved stress tolerance, especially for water or salt stress and low temperatures. The invention provides for transgenic plants with a higher level of proline accumulating ability. The invention also relates to a grass plant obtained by introducing a vector comprising a gene of the invention into a calli or protoplast derived from a grass plant, growing the calli or protoplast to obtain a colony and regenerating a plant body from the calli or colony. This sequence represents DNA encoding the rice P5CS polypeptide of the invention

CC Sequence 2549 BP; 719 A; 453 C; 648 G; 729 T; 0 U; 0 Other;

Query Match 100.0%; Score 2549; DB 7; Length 2549;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCTGCGCGGAGAGCGCGGAGACGTGGAGAGGAGATTTCAGGTAGAGGAGAGG 60
DB 1 GCGGCTGCGCGGAGAGCGCGGAGACGTGGAGAGGAGATTTCAGGTAGAGGAGAGG 60
QY 61 TGGAG 120
DB 61 TGGAG 120
QY 61 TGGAG 120
DB 61 TGGAG 120
QY 121 GGAGCTGCGAG 180
DB 121 GGAGCTGCGAG 180
QY 181 GACAG 240
DB 181 GACAG 240
QY 241 TGAAGCTGCGAG 300
DB 241 TGAAGCTGCGAG 300
QY 301 AGCGAG 360
DB 301 AGCGAG 360
QY 361 TGGAG 420
DB 361 TGGAG 420
QY 421 ATATGCTGCGAG 480
DB 421 ATATGCTGCGAG 480
QY 481 TGGAG 540
DB 481 TGGAG 540
QY 541 AAGTATACCAATATTTAATGAAATGATGCACTAGCACTAGCACTAGCACTAGCACT 600
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QY 601 ATTATCTGCTATATTTGAGATATGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 ATTATCTGCTATATTTGAGATATGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 AAGTATCTGCTATATTTGAGATATGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 AAGTATCTGCTATATTTGAGATATGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 AACCATCATCAAAATCATCACTATATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 AACCATCATCAAAATCATCACTATATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

QY 781 TTGAG 840
DB 781 TTGAG 840
QY 841 TGGCTTCAAAATGAG 900
DB 841 TGGCTTCAAAATGAG 900
QY 901 TTAAGTCTTCATGAG 960
DB 901 TTAAGTCTTCATGAG 960
QY 961 AATCATCTAAG 1020
DB 961 AATCATCTAAG 1020
QY 1021 ATCTACAG 1080
DB 1021 ATCTACAG 1080
QY 1081 TGGAG 1140
DB 1081 TGGAG 1140
QY 1141 TGGCTGATATGAG 1200
DB 1141 TGGCTGATATGAG 1200
QY 1201 GCGTTCAG 1260
DB 1201 GCGTTCAG 1260
QY 1261 AAAAG 1320
DB 1261 AAAAG 1320
QY 1321 TCTTAATGCTTTTGAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 TCTTAATGCTTTTGAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 GAAAG 1440
DB 1381 GAAAG 1440
QY 1441 TGCATAG 1500
DB 1441 TGCATAG 1500
QY 1501 TTAAG 1560
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DB 1621 TGGGAG 1680
QY 1681 CAAAG 1740
DB 1681 CAAAG 1740
QY 1741 CCTTACTAG 1800
DB 1741 CCTTACTAG 1800
QY 1801 TAAAG 1860
DB 1801 TAAAG 1860

Db 721 AACCATCTCAAAATCTACACCTTATATTAAGAAAAGCATGACAAAGAAATCACTT 780
 Qy 781 TTGAGACAAATCTGCTAGTAGAGAGAGCATGACAGCAAAAGTAGAGCTGCTCT 840
 Db 781 TTGAGACAAATCTGCTAGTAGAGAGAGCATGACAGCAAAAGTAGAGCTGCTCT 840
 Qy 841 TTGGCTCAAAATAGAGGACACCTGCTGCTTAACTAGGCTTGAAGATGAGAGCATTC 900
 Db 841 TTGGCTCAAAATAGAGGACACCTGCTGCTTAACTAGGCTTGAAGATGAGAGCATTC 900
 Qy 901 TTAAGTCTTCATGAGGAAAAAAATGCTACTCTCTTCAAGAAATGCGAATTTGAGG 960
 Db 901 TTAAGTCTTCATGAGGAAAAAAATGCTACTCTCTTCAAGAAATGCGAATTTGAGG 960
 Qy 961 AATCATCTAAGAGATGATGCTGCTGAGATGCTGCTGCGCAAGAGATTTTCAAGG 1020
 Db 961 AATCATCTAAGAGATGATGCTGCTGAGATGCTGCTGCGCAAGAGATTTTCAAGG 1020
 Qy 1021 ATCTACAGAAATTTGCTACAGAGACGAAAAAGATTTGCTAGATGCTGAGATGCTT 1080
 Db 1021 ATCTACAGAAATTTGCTACAGAGACGAAAAAGATTTGCTAGATGCTGAGATGCTT 1080
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 Db 1141 TTGCTGATGAGAGGCTTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 1200
 Qy 1201 GCTTTCAGAAATCTATTTGCTACCTTGTGCAATATGAGAGACCTATTAACCAATCTTA 1260
 Db 1201 GCTTTCAGAAATCTATTTGCTACCTTGTGCAATATGAGAGACCTATTAACCAATCTTA 1260
 Qy 1261 AAAAGACAGAGGCTGCTGATGATTTAGTCTTGAAGAAACATCTGCGCCATGAGGTTG 1320
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 Qy 1321 TCTTAATGTTTGTAGTCCGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 Db 1321 TCTTAATGTTTGTAGTCCGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 Qy 1381 GAAAGTGTATGCTGCTTCTCTAAAGGTGAGAAAGAGCTATGATCAACCAATAT 1440
 Db 1381 GAAAGTGTATGCTGCTTCTCTAAAGGTGAGAAAGAGCTATGATCAACCAATAT 1440
 Qy 1441 TGCATPAGATTAATGATGCTATCTCTGTAATGTTGGTGAAGAACTTATGAGCTTG 1500
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 Db 1501 TTACACATPAGATGATGCTGATGCTGTAAGCTTGTATGATGCTGATGCTGCTGCTA 1560
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 Db 1621 TTGGCATGCTGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 Qy 1681 CAAACCTATATGTAATGATGCAAAAGCTGATTCGCGAGGCTGCAATGCAATGAGGA 1740
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 Db 1741 CTTACTAGATTCATPAGATCTTATGAGAGCTGCAAGGCTTGAAGCAATATGATGACAC 1800
 Qy 1801 TAAACACGAGAGATTAATATTTATGCTGAGCACTATGCGCAAAAGCTGCGGATTC 1860

Db 1801 TAAACACGAGAGATTAATATTTATGCTGAGCACTATGCGCAAAAGCTGCGGATTC 1860
 Qy 1861 CAAAGCTGTTTCAATTCATTCATGAGATTAAGTCTAATGAGCTGCACTGTTGTTG 1920
 Db 1861 CAAAGCTGTTTCAATTCATTCATGAGATTAAGTCTAATGAGCTGCACTGTTGTTG 1920
 Qy 1921 ATGATGCTCAATTCAGCAATTCAGCAATTCATTCATTCATTCATTCATTCATTCAT 1980
 Db 1921 ATGATGCTCAATTCAGCAATTCAGCAATTCATTCATTCATTCATTCATTCATTCAT 1980
 Qy 1981 TCGTCACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 Db 1981 TCGTCACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 Qy 2041 TATTCATATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 Db 2041 TATTCATATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 Qy 2101 TTGGCATPAGCAAGAGGCTATCCATGCGCTGGAACAGAGGCTGTTGAAGTCTCTTAA 2160
 Db 2101 TTGGCATPAGCAAGAGGCTATCCATGCGCTGGAACAGAGGCTGTTGAAGTCTCTTAA 2160
 Qy 2161 CTACACAGATGATCTTGGAGAGAGCTGAGAGAGTGAATGAGAGAGAGAGAGAGAGAG 2220
 Db 2161 CTACACAGATGATCTTGGAGAGAGCTGAGAGAGTGAATGAGAGAGAGAGAGAGAGAG 2220
 Qy 2221 ACACCATPAGAGATCTTCTTGTGCAATGAGGTCAAATGCTCTTTAGCCCTGTTCAAGAG 2280
 Db 2221 ACACCATPAGAGATCTTCTTGTGCAATGAGGTCAAATGCTCTTTAGCCCTGTTCAAGAG 2280
 Qy 2281 TNGTGATATCTCTTTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
 Db 2281 TNGTGATATCTCTTTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
 Qy 2341 CTTATGCGGCACTTCCAGATGATTTGATTTGAGGAGTCCCACTTCAATGAGCAC 2400
 Db 2341 CTTATGCGGCACTTCCAGATGATTTGATTTGAGGAGTCCCACTTCAATGAGCAC 2400
 Qy 2401 CAAAAATTAATTCATGATGCTGAGAGCAAGATTTGAGAGTGAAGTCTTCCATGAT 2460
 Db 2401 CAAAAATTAATTCATGATGCTGAGAGCAAGATTTGAGAGTGAAGTCTTCCATGAT 2460
 Qy 2461 AAGTAAATTCAGTCTGAGAGCTTGTAGCAAGAGCTATGCTGATGATGAGCAT 2520
 Db 2461 AAGTAAATTCAGTCTGAGAGCTTGTAGCAAGAGCTATGCTGATGATGAGCAT 2520
 Qy 2521 ACTAACATCTGATGATGCAATATCTAA 2549
 Db 2521 ACTAACATCTGATGATGCAATATCTAA 2549
 RESULT 3
 ABZ14061
 ID ABZ14061 standard; DNA; 2181 BP.
 XX
 AC ABZ14061;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1866.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN W0200216655-A2.
 XX
 XX 28-FEB-2002.
 PD 24-AUG-2001; 2001W0-US026685.
 XX
 PF 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.

PR 22-JUN-2001; 2001US-030011P.
XX (SCRT) SCRIIPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.

PS Claim 11; SEQ ID NO 1866; 577bp + Sequence Listing; English.

CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stresses. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office

XX Sequence 2181 BP; 624 A; 406 C; 555 G; 596 T; 0 U; 0 Other;

Query Match 43.0%; Score 1096; DB 6; Length 2181;
Best Local Similarity 69.4%; Pred. No. 2.5e-304;
Matches 1489; Conservative 0; Mismatches 655; Indels 0; Gaps 0;

QY 99 ATGGGAGAGCTGACCCGCTCCGAGCTTGTGAGAGGAGCTGAAGGCTCATCATCAAG 158
DB 1 ATATACGAGATCATGCTTACCGCGCTTGCCAAAGAGCTTAAGGCTATCGTCTCAAG 60
QY 159 GTGGGAGAGCTGACCTGCTCCAGACAAGATGAAAGTGGCTTTGGGAGGGTGGAGCT 218
DB 61 GTTGGGAGCTGACCTGCTCCAGACAAGATGAAAGTGGCTTTGGGAGGGTGGAGCT 120
QY 219 CTGTGGGAGAGCTGAAAGATGAAAGTGGCTTTGGGAGGGTGGAGCT 278
DB 121 ATCTGTGAAGAGCTTGGGAGTAACTGAGATTTGAGGCTATTTGGTGTCACT 180
QY 279 GGTGCTGTGAGATGGGAGCAGCACTAGGTACCGAAGCTTGTCAATAGCACTT 338
DB 181 GGTGCGGTGTGTGGTGTGCAAGAGCTTGTCAATAGTCAAGCAAGCTT 240
QY 339 GGTGATCTGAAAGCAAGATGAGATTTGAGAAAGCTTTGGCGCTTGTGTCA 398
DB 241 GCAGATTTGAGAGCAGCAAGATGAGATTTGAGAAAGCTTTGGCGCTTGTGTCA 300
QY 399 AGAGGAGCTGAGCTCTTACGATATGTTGTTAACTCAACTGATCTCTCACTCA 458
DB 301 AGGAGCTGATGCTTACTATGAGATCTATGTTGAGCAAGTGTGAGCGGTGTCA 360
QY 459 CTCTTGTGACGAGCAGTGAATTTGAGAAAGCTTTGGGAGCACTCACTGAAGT 518
DB 361 ATCTGTGAGCAGATGAGATTTGAGAAAGCTTTGAGAAAGCTTTGAGTGAAT 420
QY 519 GTTGAAGCATTTAATGATCTTAAAGTTAATCAATTTAATGAAATGATGCACTCA 578
DB 421 GTCAAGAGATGCTGAGATGAGAGTATTCAGGTTTCAATGAGAAATGCTATTAAC 480
QY 579 ACTGAAAGGCTCCATGATGAGATTTCACTGTGATATTTGGGATATATACAGCTTAAGC 638
DB 481 ACTGCGAGAGCCCTCAAGAGTCTACTGTATATTTGGGATATATACAGCTTAAGC 540
QY 639 GAGCTGTGAGCACTGAGATGAGAAAGCTGATCTTATTTCTGCTGATGATGAGTGG 698
DB 541 GCTCTCTGTCGCTAGAGCTGAAAGCTGATCTTTATTTCTTAAATGATGATGAGGCT 600

QY 699 TTGTATAGTGTCCACCAAGTGAACATCATCAAAATCATATCACTTATTAAGAA 758
DB 601 CTATACATGAGCTCCCAAGTGAATCTTCAAAATTAATCAACATTCATTAAGAA 660
QY 759 AAGCATGAGCAAGAAATCACTTTTGAGACAATCTGCTAGGTAGAGAGGATGACA 818
DB 661 AAACACGAGAGCAGATTAATCTTTGGCGAAAGTCAAAATTAAGACAGAGGGGATGACT 720
QY 819 GCAGAAAGTGAAGCTGCTGCTTCTGCTTCAATATGCGGACACCTGTGTTATTAAGT 878
DB 721 GCAAAAGTTAAAGTGTGTTAATGAGCTTAATGAGTGGCGCTTCTGTTATCATTAACAGT 780
QY 879 GGGTTGAAATCGAGACATCTTAAGTCTTCAATGAGGAGAAATTTGTAATCTCTT 938
DB 781 GGATATGAGCTGAGATTAATTAAGATCTTAAGAGATCGGCTGTGTGATCCCTTTC 840
QY 939 CACAAAGATGCAATTTTGGGAAATCATCTAAGAGTCTTACTGCTGATGAGCTGTT 998
DB 841 CATCAAGTGTCTATTTATGAGGCTCCGCTGTAGATCTACTTCTGTCATGAGCAGT 900
QY 999 GCGGCAAGATTTGTCAGAGCATCTACAGAAATTTGTCATCAGAGAGCAAGAAAGATA 1058
DB 901 GCTGAAAGGAAAGCTCAAGAAAGCTTCAAGCTTATCTTCAAGAAATGAGAAATTA 960
QY 1059 TTGCTAGATGTTGAGATGCTTTGAGGCAATGAGATTTAATAGCTTGAATGAA 1118
DB 961 CTACACGACATTTGCAATGCGCTTGAAGTAAATGAGAAACATTAAGCTGAGAAATGAT 1020
QY 1119 GCTATGATGCTGGGCGCAAGTGTGCTGATATGAGAAAGCTTTGTTGTAATGACT 1178
DB 1021 TTAATGATGCTGAGACAGAAAGCTGAGATTAAGATCTTTGTAAGCTGCTTATGTT 1080
QY 1179 ATAAACAGAGAAAGATGAGAGAGCTTCAAAATCTATTTGTAATCTTCAAAATGAGAA 1238
DB 1081 ATGAAGCTGAGAGATCTCAAGCTTCAAGCTTCTGCTGAGCTAAGCGAAATGAA 1140
QY 1239 GACCTTAAACAGATTAATTAAGACAGAGTGTGATGATTTAGTTAGTTAGAAA 1298
DB 1141 GATCAATAGGCTGCTGATTAAGAAACATCAAGTTCAGATGATCTTAATTTAGAAAG 1200
QY 1299 ACATCTTGCCATAGAGTGTCTTAAATTTGTTTGAAGCCGAGCTGAGCTGTTGTT 1358
DB 1201 ACTCATACCAATAGAGTGTCTTGAATTTGTTGAAATCCGGCTGATGACCTGTT 1260
QY 1359 CAGATGATCTTGGCAATTTGAGATGATGATGATGATGATGATGATGATGATGAT 1418
DB 1261 CAGGATCTTGGCTGCAATCCGAGAGTGAATGATGATGATGATGATGATGATGAT 1320
QY 1419 GCTATCAGATCAACAGATTAATGCAATAGTATTAATGATGATGATGATGATGAT 1478
DB 1321 GCTGCTGATCAATAGCTATCTTACAGAGTATCACTATGCAATTCGAGAGCTGTT 1380
QY 1479 GGTGAAATCTTATGAGCTTGTATCACTAGATGATGATGATGATGATGATGAT 1538
DB 1381 GAGGATTAATCATAGAGCTTGTGATCTCAAGAGAGAGATTCCTGATTTGCTCAAGCT 1440
QY 1539 GATGATGATGATCTTGTGATCTTCACTCAAGAGAGAGATTAATGATGATGATGAT 1598
DB 1441 GATGATGATGATCTTGTGATCTTCACTCAAGAGAGAGATTAATGATGATGAT 1500
QY 1599 GCGTCAATAGATCTGCTGCTTGTGAGATGATGATGATGATGATGATGATGAT 1658
DB 1501 AACTGAGAAATCCAGAGCTGAGGATGATGATGATGATGATGATGATGATGAT 1560
QY 1659 AATTCAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1718
DB 1561 AAGTCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1719 GCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1778
DB 1621 GCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1779 CTGACGACATATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1838

Db 1681 CTCGATGCTTATTATTTATGTTCTGCAACCAAGCCGCTACTTGTGTGGCCCAAGA 1740
 Qy 1839 GCGCAACAAGCTGGGATTTCCAAAAGCTGTTTCATTTCATGAGTATGTTCTATG 1898
 Db 1741 GCAAGTGCACAACTGGAATTTCCGGAACAAATTCATTTCACGAGTACAGTTCCAG 1800
 Qy 1899 GCTTCGACTGTTGAGTTGTTGATGATGTTCAATCAGCAATTCACATTCATGTTAT 1958
 Db 1801 GCTTCGACCGTTGAATTTGTAAGACGTAATGTTGTTATGATTCATTCACCAACAT 1860
 Qy 1959 GGAATGCTCAATACGATTTATGCTCACTACAGATGATGATGAGAGAGACTTTCTA 2018
 Db 1861 GGAATGCAACACTGATTTGCTGATGATGACGGAATGATGATGAGAGAAATTTCTTC 1920
 Qy 2019 CGCAGATTTGATGATGCTGCTGATTTGATTAATGATGATGATGATGATGATGATGAT 2078
 Db 1921 CGCAGATTTGATGATGCTGCTGATTTGATTAATGATGATGATGATGATGATGATGAT 1980
 Qy 2079 CGTTTGAATTTGATGATGCTGCTGATTTGATTAATGATGATGATGATGATGATGATGAT 2138
 Db 1981 AGGTTGGAATTTGATGATGCTGCTGATTTGATTAATGATGATGATGATGATGATGATGAT 2040
 Qy 2139 GTGGTGTGTAAGTCTCTTAATACTACAGATGATGATGATGATGATGATGATGATGATG 2198
 Db 2041 GTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
 Qy 2199 AATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2242
 Db 2101 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2144

RESULT 4

AA068841 ID AA068841 standard, cDNA, 2417 BP.

AA068841;

07-APR-1995 (first entry)

Delta-pyrroline-5-carboxylate synthetase (P5CS) coding sequence.

Delta-pyrroline-5-carboxylate synthetase; P5CS; proline; crop;

biosynthesis; metabolism; sodium chloride; salt; NaCl; drought; ds.

Vigna aconitifolia.

Key Location/Qualifiers

FT CDS 37..2052 /tag= a /product= "Delta-pyrroline-5-carboxylate synthetase"

US5344923-A.

06-SEP-1994.

29-SEP-1992, 92US-00953695.

29-SEP-1992, 92US-00953695.

(OHIS) UNIV OHIO STATE RES FOUND.

PA Delaney AJ, Verma DPS, Hu CA,

PI Delaney AJ, Verma DPS, Hu CA,

XX WPI, 1994-285533/35.

DR P-PSDB; AAR61135.

XX cDNA clone encoding bifunctional enzyme for proline prodn - useful to

PT prepare transgenic drought resistant plants.

XX claim 1, Fig 1, 17pp; English.

XX Delta-pyrroline-5-carboxylate synthetase (P5CS), catalyses the first two

CC steps in proline production in plants. By introduction into a plant of a
 CC P5CS cDNA clone, over production of proline is incurred resulting in
 CC increased sodium chloride tolerance and drought resistance. The method
 CC may be used to enhance crop performance under conditions of salt and
 CC drought stress
 XX

SO Sequence 2417 BP; 695 A; 445 C; 582 G; 695 T; 0 U; 0 Other;

Query Match 42.9%; Score 1092.8; DB 2; Length 2417;

Best Local Similarity 70.9%; Pred. No. 2.2e-303; Mismatches 617; Indels 6; Gaps 5;

Matches 1519; Conservative 0;

Qy 108 GTGCAACCGTCCCGAGGCTTGGTGGAGGAGCGGATCATCATAGGTGGGCACT 167

Db 49 GTGATCTCTTCGGGGGTTCAATGAGACGTAAGCGTGTGATCATCAAGTTGGCAAC 108

Qy 168 GGAATTTCTCAGACAAAGATGAAAGATTTGCTTGGGCAAGGTTGAGCTCTGTCCAG 227

Db 109 GCGGTGTCACTCGGGAAGAAAGAGTTAGCGGTTGGAAGATTTGGAGCTCTGTCCAG 168

Qy 228 CAGTTAAGAACTGAATCTTTAGATACGAAGATTTTGTACCTCAGGTGCTGT 287

Db 169 CAGATTAAGAACTGAATCTTTAGATACGAAGATTTTGTACCTCAGGTGCTGT 228

Qy 288 GGAATGGGCGACAGCGATTAAGTACCGGAAGCTTGTCAATAGACCTTGTGATCTG 347

Db 229 GGAATGGGCGACAGCGATTAAGTACCGGAAGCTTGTCAATAGACCTTGTGATCTG 288

Qy 348 CAAAGCCCAATAGATTAATGAAAGGTTTGGCGCTTGTGTGAGAGTGAAGTGA 407

Db 289 CAGAAACCCCACTGAACTGACGCAAGGCTTGGCGCTTGTGTGAGAGTGAAGTGA 348

Qy 408 ATGGCTCTTACGATATGTTGTTTAAACAATGATGATGATGATGATGATGATGATGATG 467

Db 349 ATGGCTCTTACGATATGTTGTTTAAACAATGATGATGATGATGATGATGATGATGATG 408

Qy 468 ACCGACGATTTTGAACACCAAGTTCCGGGAGCACTCACTGGAAGCTTGAAGTGA 527

Db 409 ACCGACGATTTTGAACACCAAGTTCCGGGAGCACTCACTGGAAGCTTGAAGTGA 468

Qy 528 TTATTGATCTTAAGTTATATCAATATTTATGAAATGATGATGATGATGATGATGATG 587

Db 469 CTGTTGGCGCTGAAGTTATTCGGGTTCATGAGAGAGCGGTTAGTACGGAAG 528

Qy 588 GTCCTATGAGATTCATCTGTGTAATTTCTGGATTAATGACAGTTTACGAGACTGTTG 647

Db 529 GTCCTATGAGATTCATCTGTGTAATTTCTGGATTAATGACAGTTTACGAGACTGTTG 588

Qy 648 GCACTGGAATGAAAGCTGATCTGCTTATTCGCTCAGGATGAGATGAGGTTGATAGT 707

Db 589 GCTTGAAGTAAAGCCGATCTCTGTTGTTGATGATGATGATGATGATGATGATGATG 648

Qy 708 GGTCCACCAAGTGAACCATCATCAAAATCATCACTTATTAAGAAAGATCAG 767

Db 649 GGCCTCCCAAGTGAACCATCATCAAAATCATCACTTATTAAGAAAGATCAG 708

Qy 768 CAGAAATCATTTTGAACAAATCTGTTAGTGAAGGAGCATGACAGAAAGT 827

Db 709 CAGAAATCATTTTGAACAAATCTGTTAGTGAAGGAGCATGACAGAAAGT 768

Qy 828 AAGCTGCTGTTGCTTCAATTAAGCGGACACCTGTGTTATTACAAGGTTTGA 887

Db 769 AAGCTGCTGTTGCTTCAATTAAGCGGACACCTGTGTTATTACAAGGTTTGA 828

Qy 888 AATCGAGCATTTTAAATTTCTCAATGAGGAAATTTGATCTCTTCAAGAGAT 947

Db 829 CTTGAATTAATTAATTTCTCAATGAGGAAATTTGATCTCTTCAAGAGAT 888

Qy 948 GCGAATTTGAGGATCATTAAGATGTTAGTACTGAGATGAGTGTGCGGACAGA 1007

Db 889 GCAATGATGAGGCTCAAGTAAAGAGTTGATGACGTAAGATGAGTGTGCGGAC -AGG 947

Qy 1008 GATTGTTCAAGGATCTACAGAAATTTGATGAGAG -AACGAAAAAAGATTTGCTAGA 1066

Query Match 42.9%; Score 1092.8; DB 2; Length 2417;
 Best Local Similarity 70.9%; Pred. No. 2.2e-303;
 Matches 1519; Conservative 0; Mismatches 617; Indels 6; Gaps 5;

108 GTGACCCGCTCCGAGCTTGTGAGGAGCGTGAAGCCGTCATCATCATCAAGTGGGCACT 167
 49 GTGATCTCTTCGCGGGGTTATGAGAGCGTGAAGCGTGTGATCATCAAGTGGGCACT 108
 168 GCATGTTCTCCAGCAAGATGGAAGATTGGCTTTGGCAGGGTTGAGCTCTGTGGAG 227
 109 GGGTGGTCACTCGGAGAGAGAGGATTAGCGGTGGAGATTGGGAGCTCTGTGGAG 168
 228 CAGTTAAGAACTGAATCTTTAGATACGAAGATTTGGTCACTGAGTGTGTT 287
 169 CAGATTTAAGAACTGAATCTTTAGATACGAAGATTTGGTCACTGAGTGTGTT 228
 288 GAGTGGGGCGACAGCACTTAGTACCGGAGCTTGTCAATAGAGCTTGTGATCTG 347
 229 GGTATTGGACGCGCAAGGCTACGTTCCGTAAATTAACAAGAGCTTGGCGACCTT 288
 348 CAAAGCCACAGATGAGATTGATGAGAAAGCTTGGCGGCTTGTGTCAGAGTGA 407
 289 CAGAAACCCCACTGAACTCGACGCAAGCTGCGCGCTTGGAGCAGACAGTCTC 348
 408 ATGCTCTTTACGATATGTTGTTTACCAACTGATGTCTGTCACTCACTTCTTGTG 467
 349 ATGGCTCTACGATACGCTGTTCATCAAGCTCGATGTGATGGGCTCACTTCTTGTG 408
 468 ACCGACAGGATTTTGAAGACCCAAAGTTCCGGGAGCACTCACTGAAACTGTGATCA 527
 409 ACGGATTAAGATTTCAAGATTAAGATTTCAAGGAGCACTTACGACAGCTGAAAGCG 468
 528 TTATTAGATCTTAAAGTTATACCAATATTATTAAGAAATGATGCGATGAGATGAAG 587
 469 CTGTGGCGCTGAAGATTATTCGGTGTTCATGAGAGATGCGCTTATGATCAAGAG 528
 588 GCTCCATGAGGATTCATCTGTGATATTCTGGATTAATGACAGTTTGAAGAGCTGTG 647
 529 GCTCCCTTAAGAGATTTCTTGTGATATTGTTGGGAAATGATGATTATCTGCTTTATTA 588
 648 GCATGGAAGCTGAAGAGCTGATCTCTTATTTGCTCAGTGAATGGAGGGTGTGATAGT 707
 589 GCTTGGAGATTAAAGCCGATCTCTTGTGTTGTTGATGATGATGAGAGCTTTACAGT 648
 708 GGTCCACCAAGTGAACCATCATCAAAATCATACACACTTATTTAAAGAAAGCATCAG 767
 649 GGCCCTCCAGTGAACCCCTCATCAAGCTTATTTATACATATTAACAAGAAACATCAG 708
 768 CAAAGAAATCATTTGGAGACAATCTGTGTGATGATGAGAGAGAGAGAGCAAGAAAGTG 827
 709 AATGAATTAATCTTTGGGCGACAGCTTGAAGTGAAGAGGGGAAATGATGCCAAAGTA 768
 828 AAGGCTGTGTCTTGGCTTCAATAGCGGACACCTGTGTATTTACAGTGGGTTGAA 887
 769 AAGGCTGGGCTTCATGCACTGAGCTGATCTCTGTTTATTAACAAGGTTTTCACA 828
 888 AATGAGAGATTTTAAAGTTCTTCAATGGGAAAAATTTGTATCTCTTTCAACAAGAT 947
 829 CCGAATAATCATTAATGTTCTTCCAGAGCAACGATATAGAACTCTTCCATTAAGAT 888
 948 GCGAATTTGGGAATCATCTAAGATGTTTATGATCTGAGATGAGCTGTGGCGCAAGA 1007
 889 GCAATGATGAGGCTCAATTAAGAGTGTATGACGATGATGGCTGTGGAGC AGG 947
 1008 GATTGTTCAAGGATTTACGAATTTGTATCAAGAG -AAGAAAAAGATTTGTCTAGA 1066
 948 GATGTTTCAGAAAGGCTCCAGCGTATCTTCAAGAGAAAGAAACAAATTTTACTTAA 1007
 1067 TGTGAGATGCTTTGAGAGCAATGAGGATTTAATTAAGTGTGAGATGAGAGCTGATGT 1126
 1008 AATAGCTGATGCCCTGAGAGCAATGAAAAAATTAATCAGATTTGAAAAAGCTGATGT 1067
 1127 AGCTGCGGCCCAAGTGTGATGATGAGAAAGCTTGTGTTGCTAGATGATTAATAACG 1186

1068 TATCTGTGACAAAGAGCAGATATGAAAAATCTTGGTGGTATGAGCTTATTAACCC 1127
 1187 AGGAAGATAGCAAGGCTTGCAGAAATCTAATGTAACCTTGCAGAAATAGAGACCTAT 1246
 1128 TGGAGAGATTGCAAGCTTGCAGAAACATGGAATCATATGCAATATGAGATCCAT 1187
 1247 AAACGATATCTTAAAGAACAGAGGTGTGATGATTTAGTCTTGAAGAAACATCTTG 1306
 1188 TGGTCAAGTATTAACAGTACCGAGCTTCAATGAGGCTTAATTTAGAAAAACATCATC 1247
 1307 CCCATAGGTTCTCTTATTTGATGATCCGACCTGATGCTTGTCAATATGAC 1366
 1248 TCCCTTGGAGAGTCTCTTATTTGATGATGATGATGATGATGATGATGATGATGATG 1307
 1367 ATCTTGGCAATTCAGAGTGTATGCTTCTCTTAAAGGTGAAAGAAAGCTATCAG 1426
 1308 TTCAATGGCAATCCGAGAGGGAATGGGCTTCTTGAAGAGTGGCAAGAGCTAAGCG 1367
 1427 ATCAACAGATATTCATAGATTATTAATGATGATATCTCGTAAATGTTGATGA 1486
 1368 ATCAATATGATTTTGAACAAAGTATTTATGAGGCTATCCAGATATGTTGGTGA 1427
 1487 ACTTATGAGCTTGTATCAACTAGAGATGATGCAATTTGCTPAAAGCTTATGATGT 1546
 1428 ACTTATGAGCTTGTATCAACTAGAGATGATGCAATTTGCTPAAAGCTTATGATGT 1487
 1547 CATGATCTTGTCACTCCAGAGGAAATTAAGCTTGTCTCAATCAAGGCTCAAC 1606
 1488 AATGATCTGATATTCAGAGGAGATTAACAACTGTTTCTTCAAGTCAAGATTTCAAC 1547
 1607 TAAATTCCTGTTTGTGGCATGCTGATGATGATGATGATGATGATGATGATGATGATG 1666
 1548 TAAATTCCTGTTTGTGGCATGCTGATGATGATGATGATGATGATGATGATGATGATG 1607
 1667 TGAATGATATGAGCAAACTTATTTGATGATGATGATGATGATGATGATGATGATGATG 1726
 1608 TAACTGAGATGAGCAAACTTATTTGATGATGATGATGATGATGATGATGATGATGATG 1667
 1727 CATGCAATGAGACCTTACTAGTATGATGATGATGATGATGATGATGATGATGATGATG 1786
 1668 CATGCAATGAGAACTTACTAGTATGATGATGATGATGATGATGATGATGATGATGATG 1727
 1787 CATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1846
 1728 GATCATCTTGTGACCTTCAAGAGGCTTATTTATTTATTTATTTATTTATTTATTTAT 1787
 1847 AGCTTGGGATTTCCAAAGGCTTTCATTTATGATGATGATGATGATGATGATGATGATGAT 1906
 1788 TCTGTTAATATTTCCAGAGCACTTATTTATGATGATGATGATGATGATGATGATGATGAT 1847
 1907 TGTGAGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1966
 1848 CGCGAAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1907
 1967 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2026
 1908 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1967
 2027 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2085
 1968 AGACAGTGTGCTGTTTTCATCAATGATGATGATGATGATGATGATGATGATGATGATG 2027
 2086 GATTGGTGTGAGTTGGCATGAGACAGGCGTATTCATGATCCGTGAGCAAGTGGG 2145
 2028 GACTAGGCGAGAGGTTGAAATTTAGTAAAGAGATTTATGATGATGATGATGATGATGAT 2085
 2146 TGAAGGCTCTTAACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2205
 2086 GTTGAAGATTTTAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2144
 2206 ACAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2247

Db 2145 ATAGAGCGCTTCTACACCCAGAGAGACCTTGCAATTAAAT 2186

RESULT 6
ID AB213586 standard; DNA; 2154 BP.
AC AB213586;
XX
XX 21-JAN-2003 (first entry)
XX
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1391.
DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
XX Arabidopsis thaliana.
OS
XX MO200216655-A2.
XX
XX 26-FEB-2002.
XX
XX 24-AUG-2001; 2001MO-US026685.
XX
XX 24-AUG-2000; 2000US-0227866P.
XX 26-JAN-2001; 2001US-0264647P.
XX 22-JUN-2001; 2001US-0300111P.
XX
XX (SCRI) SCRIPS RES INST.
XX (SYN) SYNGENTA PARTICIPATIONS AG.
XX
XX Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
XX
XX Claim 15; SEQ ID NO 1391; 577bp + Sequence Listing; English.
XX
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
XX Sequence 2154 BP; 595 A; 412 C; 562 G; 585 T; 0 U; 0 Other;

Query Match 42.6%; Score 1085.6; DB 6; Length 2154;
Best local similarity 69.1%; Pred. No. 2.5e-301;
Matches 1484; Conservative 0; Mismatches 664; Indels 0; Gaps 0;

QY 99 ATGCGAGCGTGAACCGGCTCCGAGCTTCGTGAGGAGCGTGAAGCGCTCATCATCAAG 158
DB 1 ATGAGAGGAGCTAGATCGTTCACGTCTTTTCCAGAGACGTCAACGTATCGCTTAAAG 60
QY 159 GTGGGCACTGAGCTGCTCTCCAGACAGATGAGAGATTTGGCTTTGGGCAAGGTTGAGCT 218
DB 61 GTTGGACAGCAGTGTGTACTGTGAAAGGTGAAAGATTTGGCTTTGGCTTTGAGAGCA 120
QY 219 CTGTGCGAGCAGCTTAAAGACTGAACTTTAGATGAGATGAGATGATTTGGTCACTCA 278
DB 121 CTGTGTGAACAGCTTGGGGAATTAACCTCGATGATTTGAGGATGATTTGGTCACTC 180
QY 279 GGTGCTGTGAGAGTGGGCGACAGCACTTATGATACCGGAAGCTTGCAATACAGCTTT 338
DB 181 GGTGCGTGTGTCTTGGAGGCAAGGCTTGTATGACATTAATGACATGAGCTTT 240

QY 339 GGTGATCTGCAAAAGCCACAGATGAGATGATGAAAGGCTTGTGCCCTTTGTGAC 398
DB 241 GCGATCTTTCAGAAAGCCCTCAGACGTGAACCTTGATGGAGGCTTGTGTGTGGACAA 300
QY 399 AGTGACTGATGAGCTCTTACGATATGTTTAAACCACTGATGTCTGCTCATCTCAA 458
DB 301 AGCAGCTTAAGGCTTACTATGAGATATGTTTGAACGAGCTTATGAGGCGAGCTCAA 360
QY 459 CTTCTGTGACCGACAGTGAATTTTGAAGCCCAAGTTCCGGAGCACTCACTGAACT 518
DB 361 CTTCTGTGATGACAGTATGTTTGAAGACAGGATTTCCAGGAAGCACTTAATGAAACT 420
QY 519 GTTGAATATTAATGATCTTAAAGTTAAACCAATATTTATGAAATGATGATCAAGC 578
DB 421 GTCAAGTCTAAGCTTGTATTTGAGGCTTATTCATATTTCAATGAGATGATGATAGC 480
QY 579 ACTGAAAGGCTCCATATGAGGATTCATCTGTGATATTTCTGGATPAAATGACAGTTTGA 638
DB 481 ACCGAAAGAGCCCATATCAGATTTCTTGTGATTTTCTGGATPAAACGATAGCTTACGT 540
QY 639 GACCTGTGCACTGGAACCTGAAGCTGATCTCTTATCTGCTCAGTATGATGAGTGG 698
DB 541 GCTTACTGCGCTGGAACCTGAAGCTGATCTTGTATCTTCTGACGATTTGAAAGCT 600
QY 699 TGTATAGTGTGCAACCAAGTGAACCATCATCAAAATTCATACACACTTATTTAAAGAA 758
DB 601 CTTTACAAGGCCCTCCAGATGATCTTAACCTCAAGTTGATCCACACTTTTGTAAAGAA 660
QY 759 AAGCATGCAAGAAATATCTTTTGGAGACAAATCTGTGTAGTAAAGAGGATGACA 818
DB 661 AAACATCAAGATGAGATTAATCTGGGACAAATCAAGATTTGAGAGAGGGGGATATAC 720
QY 819 GCAAAAGTGAAGGCTGCTCTTGTGCTTCAATATGCGGACACCTGTGTATTTACAAAGT 878
DB 721 GCAAAAGTGAAGGCTGCTCTTGTGCTTCAATATGCGGACACCTGTGTATTTACAAAGT 878
QY 879 GGGTTTGAAGGCTGCTCTTGTGCTTCAATATGCGGACACCTGTGTATTTACAAAGT 938
DB 781 GGGTTTGAAGGCTGCTCTTGTGCTTCAATATGCGGACACCTGTGTATTTACAAAGT 840
QY 939 CACAAGATGCGAATTTTGGGAAATCATCTAAGAGTGTAGTACTGAGAGATGGCTGT 998
DB 841 CATCAAGATGCTGCTTATGAGGCTTCCATCCATCAAGATTTATGCTGATGATGGCAGT 900
QY 999 GCGGCAAGATTTGTTCAAGGCAATCAAGATTTGCTATGACAGAAACGAAAGATA 1058
DB 901 GGTGAGAGGAAAGTTCCAGAAAGCTTCAAGGCTTATCTTGGAAAGACAGGAAAGAAATT 960
QY 1059 TTGCTAGATGTTGAGAGATCTTGGAGCAATGAGATTAATTAAGGCTGAGATGAA 1118
DB 961 CTGCTGATATTTGCGAGATGCTTGGAGCAATGAGATTAATTAAGGCTGAGATGAA 1020
QY 1119 GGTGATGATGCTGCGGCAAGTGTCTGATATGAGAAAGCTTTGTTGCTAGATGACT 1178
DB 1021 TTAGATGATGCTTTCGACAAAGAGGCTGTTGAAAGATCAATGTTGCTGCTGATGTT 1080
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DB 1081 ATGACACCTGGAAGATTTGAGGCTTGCACCTTCAAGTCTTAAGCTGATGATGAGAA 1140
QY 1239 GACCTATTAACAGATATCTTAAAGACAGAGTGTGATGATTAATGTTTGAAGAA 1298
DB 1141 GATCAATCGGCGGTGTTTAAAGAAACAGAGGTGAGATGATGCTTGTATGAGAAAG 1200
QY 1299 AATCTTGGCCATTAAGTGTCTCTTAATGTTTGAATGCCAAGCTGATGCTTGGTT 1358
DB 1201 AACTCATCAACATTAAGGCTTCTGATGTTTGAATGCCAAGCTGATGCTTGTATA 1260
QY 1359 CAGATTGATCTTTGGCAATTCGAAGTGTATGCTTCTCTTAAAGGTGAGAAAGAA 1418
DB 1261 CAGATAGCTTACCTTGCATCCGTATGAGTGAATGCTTCTGCTGAGAGGGTGAAGAGAG 1320

PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144335P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145182P.
PR 23-JUL-1999; 99US-0145182P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147433P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
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PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151103P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.

PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0156599P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161358P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161932P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 42.6%; Score 1085.6; DB 3; Length 2273;
Best Local Similarity 69.1%; Pred. No. 2,66-301;
Matches 1484; Conservative 0; Mismatches 664; Indels 0; Gaps 0;

QY 99 ATGGCAGCGTCGACCCGCTCCGAGCTTGGTGGAGCAGTGAACCGCGTCATCATGAC 158
DB 120 ATGGAGAGCTAGATCGTTCACGCTTTGCCAGACGCAACGATATCGTGTAAAG 179
QY 159 GTGGGCACTGAGTGTGTCTCCAGACAGATGGAAGATTGGCTTTGGCAGGTTGAGCT 218
DB 180 GTGGAGAGCAGTGTGTCTCCAGACAGATGGAAGATTGGCTTTGGTGTGTTGAGACA 239
QY 219 CTGTGCGAGCAGGTTAAGAACTGAACTCTTTAGATACGAAGTGAATTTGGTCACTCA 278
DB 240 CTGTGTAAACAGCTTGGGAGATTAACTCGGATGATTGGTGGATATTGGTCTACTCT 299
QY 279 GGTGCTGTGAGAGTGGGCGGACAGCGACTTAAGTACCGGAAGCTTGCATATAGAGCTT 338
DB 300 GGTGCGTGTGTCTTGGAGGCAAGGCTTGTATGACAAATTAAGTCAATAGAGCTT 359
QY 339 GCTGATCTGCAAAAGCCACAGATGAGTATGATGAAGGCTTGTGCGCTGTGTGACAG 398
DB 360 GCGGATCTTCAAGAGCCACAGCTGAATGATGGAAGGCTTGTGCGGTGTGACAA 419
QY 399 AGTGACTGATGGCTCTTTAGATATGTGTTTAACTGATGATGCTTGTCTGTATCTCAA 458
DB 420 AGCAGCTTATGAGCTTACTATGAGACTATGTTTACCAAGCTTGTATGAGCGGAGCTCAA 479
QY 459 CTTCTGTGACCGCAGAGTATTTGAGAACCCAAAGTTCGCGGAGCACTCACTGAAGT 518
DB 480 CTTCTGTGATGACAGAGTATTTAGAGCAAGATTTTCAAGAGCAACTTAATGAACT 539

QY	519	GTGTAGTCATTAATAGACTCTTAAGATTAATACCAATATTAAATGAATGATGCATGAG	578
Db	540	GTCAAGCTATAGCTTGATTTGAGGGTATTTCCAATTTTCAATGGAATGATGCTATTAGC	599
QY	579	ACTAGAAAGGCTCCATATAGAGATTCAATCTGGATATTTCTGGGATTAATGACAGTTTAGCA	638
Db	600	ACCCGAGAGAGCCCATATCAAGATTCTCTGGTATTTTCTGGGATTAACGATACCTTAGCT	659
QY	639	GGACTGTGGACCTGGGAAGCTGAAGAGTATGCTCTTAATTCGCTCAGTGATGAGATGGG	698
Db	660	GCTTACTGGGCTTTGGAACTGAAGCTGATTTCTTGATTTCTTGAGGATGTTGAAGCT	719
QY	699	TTGTATAGTGTCCACCAAGTGAACCATCATCAAAAAATCATACACACTTATATTAAAGAA	758
Db	720	CTTTACACAGGCCCTCCAGATGATCTTAATCAAAAGTTGATCCACACTTTGTTAAAGAA	779
QY	759	AAGCATCAGCAGAAATATCACTTTTGGAGACAAATCTCGTGTATAGGTAAAGAGCATACCA	818
Db	780	AAACATCAAGATGATGATTAACATTTGGCGACAAATCAAGATTAGGAGAGGGGGATATAC	839
QY	819	GCAAAAGTGAAGGCTGCTGTCTTGAGCTTCAATATAGCGGACACCTGTGTATTATACAGT	878
Db	840	GCAAAAGTCAAGCTGACGATCAATGACAGCTTATGCTGGGATTCCTGTCAATATACCAAGT	899
QY	879	GGGTTTGAATTCGAGACATTCTTAAGTTCTTATGGGGAATAATTTGGTACTCTCTTT	938
Db	900	GGGTATTCAGCTGAGAACATGATGAATAAGTCTCCAGAGACATACGTTGTGAACCTTGTT	959
QY	939	CACAAAGATGGCAATTTGTGGGAATCAATCTAAGATGTTATACCTCGGAGATGCGTGT	998
Db	960	CATCAAGATGCTCGTTTATGGGCTCCGATCAACAATTTATAGCTGTGACATGSCAGTT	1019
QY	999	GCCGCAAGAGATTGTCAAGGCATCTACAGAAATTTGTATCAGAGGAACGAAAAAGATA	1058
Db	1020	GCTCGAGAGGAAAGTTCCAGAAAGCTTATCAGGCTTATCTTGGAAAGACAGAAAAAATT	1079
QY	1059	TTTGTATAGTGTGACAGATGCTTTGGAGCAATATGAGATTAAATAGTCTGAATATGAA	1118
Db	1080	CTGCTGTATATTCGCGATGCGCTTGAAACCAATGTACTACATCAAGCTGGAATATGAG	1139
QY	1119	GCTGATGATGCTGGGCCCAAGTTGCTGGATATGAGAACCTTTGGTGTCTAGATTGACT	1178
Db	1140	TTAGTGTAGTTCCTGCAACAGAGGCTGGTTGGAAAGTCAAGATGTGTGCTGCTTAGTT	1199
QY	1179	ATTAACACAGAAAGATGACAGCTCTTGCAAAATCTATTTGTAACCTTGCAAAATATGGA	1238
Db	1200	ATGACACTTGAAAGATCTCGAGCCTTGCACTTCAGTTCTTAAGCTATGCTGATATGGA	1259
QY	1239	GACCTATTAACCAAGATACTTAAAAAGACAGAGTGTGATGATTAATGTTAGTCTTGAGAA	1298
Db	1260	GATCCATTCGGCCGCTTTTAAAGAAAAACAGGTGGACAGATGCTTGTCTTGAGAGAG	1319
QY	1299	ACATTTGCCCATTAAGTGTCTCTTAATGTTTTTGAATGCCACCTGATGCTTGTT	1358
Db	1320	ACCTCATCACATTAAGCGTACTTCTGATTTGTTTGAATCCCACTGATGACCTTGTA	1379
QY	1359	CAGATGTGATCTTTGGGCAATCGAAGTGTATGCTTCTCCTAAGAGGTGAAAAAGAA	1418
Db	1380	CAGATAGCTTCACTTGCCATCCGATGTGAATGTCTTCTGCTGAAGGGTGAAGAGAG	1439
QY	1419	GCTATCAGATCAAAACACGATATTTGCATTAAGGTTTAACTGATGCTATTTCTCGTATGTT	1478
Db	1440	GCCCGGCGATCAAAATGCTATCTTACACAGGATGATCACTGATGCAATTCAGAGACTGTT	1499
QY	1479	GGTGAAAAACTTATTTGGCTTGTTCACATGAGATGAGATTCGAGATTTGCTAAAGTT	1538
Db	1500	GGGGGTAACCTATTGACTGTGTGCTTCAAGAGAGAGATTCCTGATTTCTTAAGTT	1559
QY	1539	GATGATGCTATGATCTTGTCACTCAAGAGAGATAATTAAGCTTGTCTTCAATCAAG	1598
Db	1560	GATGACGTTATCGATCTTGTGTATCCCAAGAGAGACAAAGCTTGTATCTCAGATATGAA	1619
QY	1599	GGGTCACTAAGATTCCTGTTCTTGGGACATGCTGATGTGATATGCCACGTATATTTGAC	1658

Db	1620	AAATCTACAAAATACCCCTGGCTAGTGCATGCTGATGGAAATCTGTCAATGTTATGTCGAC	1679
Qy	1659	AAATCAGCTGACATGATATGCGAAAATTAATTTATATGATGCAAAAACTGATTAACCA	1718
Db	1680	AAGCTTGTTGTTACGGATATGCGAAACCGCATATGTTCTGTATGCAAACTTGACATATCCA	1739
Qy	1719	GCAGCTTGCAATGCAATGAGAGACTTCTACTAGTTATATTAAGATCTTATGAAAGTCCAGGC	1778
Db	1740	GCACCTCTGTATGCGATGCGAAACCCCTTCTTGCTGATTAAGATCTTAGAGCAGAAATGCTGTG	1799
Qy	1779	CTTGACGACATATTTAGTAGCACTTAAAAACAGAGAGATTATTTATATGTCGACTTAT	1838
Db	1800	CTTATATGAGCTTATTTTGTCTGTGCAAGCATGAGATGAGTCACTTGTATGTGGACAAAGG	1859
Qy	1839	GGCGACAAAGCTCTGGGATTTCCAAAAGCTGTTTCATTTTCATGATGATATGTTCTATG	1898
Db	1860	GCAAGTATGATCTGAAACATACGAAAGCAGCGTCACTTCAACATGATCTGTGCCAAG	1919
Qy	1899	GCCTGCACTGTGTAAGTTTGTATGATGTTCAATCAGCAATTGACCAATATTCATGTTAT	1958
Db	1920	GCTTGCACTGTGTAAGTTGTGAAAGACGTTTATGTGCTATAGATTCATTCACCGACAT	1979
Qy	1959	GGAGTGTCTCATACAGATGTATGCTCATTACATACATATGATTAAGTAGAGACACTTTCTA	2018
Db	1980	GGGAGTGACACACAGACTGCATTTGTACAGAGATCACGAAAGTTGCAGACTTATTCCTT	2039
Qy	2019	CGCAGAGTGAATGATGCTGCTGATTTTCATATATCAGATGACGAGATTCCTGATGGGCT	2078
Db	2040	CGCCAGTGGATACCGCTGCTGTCTTCCACAACCGCAGACAAATTCCTCAGATGGTTTC	2099
Qy	2079	CGTTTGGATTTGGTGTCTGAGGTTGSCATTAAGCACAGGCGTATCCATGCCCCGTGACCA	2138
Db	2100	CGATTTGGACTTGTGTGCAAGGTGGGGTAAAGCACGGCAGAGTCCATGCTGTGATCCA	2159
Qy	2139	GTGGGTGTGTAAGGTCTCTTAACTACACAGATGATCTTTCGAGAGACGTGGGCAATGGTGTG	2198
Db	2160	GTCGGGGTGCAGAGATTACTTACAAACAGATGATATGATGAGAGAAAAGCAAGTTGTC	2219
Qy	2199	AATGATGACAAAGATGTGCTGTACACCCCATTAAGAGTCTTCTTTGCCA	2246
Db	2220	GACGAGACATGGAATTTGTACACCCATCAGACATTCCTCCATCCAA	2267
RESULT 8			
ABX93778			
ID	ABX93778	standard; cDNA; 2571 BP.	
XX	AC	ABX93778;	
XX	DT	17-JUN-2003 (first entry)	
XX	DE	Thale cress delta^1-pyrroline-5-carboxylate synthetase (P5CS) cDNA.	
XX	KM	Grass; delta^1-pyrroline-5-carboxylate synthetase; P5CS; gene; ss;	
XX	KM	proline dehydrogenase; PRODH; stress tolerance; water tolerance; calli;	
XX	KM	salt stress; salinity tolerance; temperature tolerance; protoplast;	
XX	KM	proline accumulation; thale cress.	
OS	Arabidopsis thaliana.		
XX	Key	Location/Qualifiers	
XX	CDS	107..2260	
XX	FT	/*tag= a	
XX	FT	/product= "Thale cress P5CS"	
XX	FN	GB2376236-A.	
XX	PD	11-DEC-2002.	
XX	PF	24-DEC-2001; 2001GB-00030946.	
XX	PR	08-JUN-2001; 2001JP-00174553.	

XX (HITA) HITACHI LTD.
PA (BIO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
PA (INDE-) INDEPENDENT ADMINISTRATIVE INST NAT INST.
PA (RIKE) RIKEN KK.
XX
PI Yoshida Y, Shinzaki K;
XX
DR WPI; 2003-203644/20.
DR P-PDSB; AB009030.
XX
PT New grass plant overexpressing a P5CS gene from rice, useful for making
PT transgenic plants with higher levels of proline accumulating ability, and
PT more improved salinity-tolerance, drought-tolerance and low temperature-
PT tolerance.
XX
PS Claim 2; Page 29-36; 52pp; English.
XX
XX The invention relates to a grass plant in which a delta¹-pyrroline-5-
CC carboxylate synthetase (P5CS) gene of rice, or a P5CS gene of Arabidopsis
CC thaliana and the antisense gene of a proline dehydrogenase (ProDH) gene
CC of Arabidopsis thaliana, have been introduced in tandemly connected
CC relation to each other. A new method of the present invention is useful
CC for the production of a transgenic rice plant with improved stress
CC tolerance, especially for water or salt stress and low temperatures. The
CC invention provides for transgenic plants with a higher level of proline
CC accumulating ability. The invention also relates to a grass plant
CC obtained by introducing a vector comprising a gene of the invention into
CC a calli or protoplast derived from a grass plant, growing the calli or
CC protoplast to obtain a colony and regenerating a plant body from the
CC calli or colony. This sequence represents DNA encoding the chole cress
CC P5CS polypeptide of the invention
XX
SQ Sequence 2571 BP; 698 A; 493 C; 638 G; 742 T; 0 U; 0 Other;
XX
Query Match 42.6%; Score 1085.6; DB 7; Length 2571;
Best Local Similarity 69.1%; Pred. No. 2.8e-301;
Matches 1484; Conservative 0; Mismatches 664; Indels 0; Gaps 0;
XX
QY 99 ATGCGGAGGCGTCCGCGGAGCTTCGAGGAGGAGTGAAGCGGTCATCATCAAG 158
DB 107 ATGAGAGAGCTGATGTTCAAGTGTCTTTGCGAGAGAGTCAAGATGATCGTTAG 166
QY 159 GTGGGAGAGCTGATGTTCTCCAGAGCAAGATGAGATGAGTTGGGCGAGGTTGAGCT 218
DB 167 GTTGGAGAGAGCTGATGTTCTGAGAGAGGTTGAGATGAGTTGGTCTTTAGAGACA 226
QY 219 CTGTGAGAGAGTTAAGAGAGTGAAGCTTTAGAGTGAAGTATTTGGTCACTCA 278
DB 227 CTGTGTGAAGAGTTGCGGATTTAACTGAGATGATTTGAGGTATTTGATCT 286
QY 279 GGTGCTGTGAGAGTGGGCGAGAGAGCTTAGTACCGAGCTTGTCAATAGAGCTTT 338
DB 287 GGTGCGGTGTGCTTGTGAGAGGAGAGGCTTGTATGAGCAATTTAGTCAATAGAGCTTT 346
QY 339 GGTGATCTGAGAGAGAGAGAGAGAGTGAAGTGAAGAGAGCTTGGCGGCTTGGTAG 398
DB 347 GCGGATCTTGAAGAGCTGAGAGTGAAGTGAAGAGAGCTTGGCTGGTGTGAGACA 406
QY 399 AGTGAAGTGAAGCTTTTACGATATGTTTGAAGTGAAGTGAAGTGTCTGTCACTCA 458
DB 407 AGGAGCTTATGCTTACTATAGAGCTATGTTTGAAGCTTGAAGTGAAGCTCA 466
QY 459 GTTGTGTGACAGAGAGTATTTTGAAGAGAGAGTTCGGAGAGAGTCACTGAAGT 518
DB 467 GTTGTGTGATGAGAGTATTTTGAAGAGAGAGTTCAGAGAGAGTCAATGAAGT 526
QY 519 GTTGAAGTATTTATGATCTTAAAGTATACCAATTTTAAAGAAATGATCCATAGC 578
DB 527 GTCAAGCTATGCTGATTTGAGGATTTATTCATTTTCAATGAAGATGATCTATAGC 586
QY 579 ACTGAAGAGCTCATATGAGATTCATCTGTATTTCTGGATATATACAGTTTAGA 638

DB 587 ACCGAGAGAGCCCATATGAGATCTTCTGATTTCTGGAGTAAAGATAGTTAGCT 646
QY 639 GAGCTGTGACATGAGAGAGAGAGAGAGTATCTTATCTGTGAGAGAGTATGAGTGG 698
DB 647 GCTCTACTGAGAGTGAAGAGAGAGAGAGAGTATCTTATCTTGTGAGAGAGTGAAGT 706
QY 699 TTGTATAGTGTCCAGAGAGAGAGAGAGTATCTTATCTTATCTTATCTTATGAAG 758
DB 707 CTTTACAG 766
QY 759 AAGCATGAG 818
DB 767 AAGCATGAG 826
QY 819 GCAAG 878
DB 827 GCAAG 886
QY 879 GGGTTGAG 938
DB 887 GGGTATTCAG 946
QY 939 CACAG 998
DB 947 CATAG 1006
QY 999 GCGGAG 1058
DB 1007 GCTGAG 1066
QY 1059 TTGTATAGTGTCCAG 1118
DB 1067 CTGCTGATATTCAG 1126
QY 1119 GCTGATGATGAG 1178
DB 1127 TTGATATGATGAG 1186
QY 1179 ATAAAG 1238
DB 1187 ATGACAG 1246
QY 1239 GAGCCTATTAAG 1298
DB 1247 GATCAATGAG 1306
QY 1299 ACATCTTGAG 1358
DB 1307 ACCTCATGAG 1366
QY 1359 CAGATGAG 1418
DB 1367 CAGATGAG 1426
QY 1419 GCTATGAG 1478
DB 1427 GCGGAG 1486
QY 1479 GGTGAG 1538
DB 1487 GGGGAG 1546
QY 1539 GATGATGAG 1598
DB 1547 GATGATGAG 1606
QY 1599 GCGTGAAG 1658
DB 1607 AATGATGAG 1666
QY 1659 AATGATGAG 1718
DB 1667 AAGCTGTGAG 1726

PR 20-JUL-1999; 99US-0144884P.
 PR 21-JUL-1999; 99US-0144814P.
 PR 21-JUL-1999; 99US-0145086P.
 PR 21-JUL-1999; 99US-0145088P.
 PR 22-JUL-1999; 99US-0145085P.
 PR 22-JUL-1999; 99US-0145087P.
 PR 22-JUL-1999; 99US-0145089P.
 PR 22-JUL-1999; 99US-0145192P.
 PR 23-JUL-1999; 99US-0145145P.
 PR 23-JUL-1999; 99US-0145218P.
 PR 23-JUL-1999; 99US-0145224P.
 PR 26-JUL-1999; 99US-0145276P.
 PR 27-JUL-1999; 99US-0145213P.
 PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145851P.
 PR 02-AUG-1999; 99US-0146386P.
 PR 02-AUG-1999; 99US-0146388P.
 PR 03-AUG-1999; 99US-0146389P.
 PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147204P.
 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147322P.
 PR 05-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147433P.
 PR 09-AUG-1999; 99US-0147935P.
 PR 10-AUG-1999; 99US-0148171P.
 PR 11-AUG-1999; 99US-0148319P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 13-AUG-1999; 99US-0148684P.
 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154759P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 04-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.

PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159658P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160777P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160960P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 24.3%; Score 619.8; DB 3; Length 1343;
 Best Local Similarity 71.6%; Pred. No. 2; e-167;
 Matches 813; Conservative 0; Mismatches 322; Indels 0; Gaps 0;

DB 1108 CTGAGATGAAGCTGATGTAGTGCAGCCCAAGTTCGTGATATGAGAACCTTTGGTTG 1167
 7 CTGAGATGATTTAGATGTTGTGCAGCACAAGAGCTGATATGAGAGCTTTGGTGG 66
 QY 1168 CTGATTTGACTTAAACCGAGAAAGATAGCAAGCTTTGAAATCTATTCTGACCTTG 1227
 DB 67 CTCGCTTATGATTAAGACCTCGGAGAGATCAAGCTTCGAGCTTCGTTGCGACCTGAG 126
 QY 1228 CAAATATGAGAGACCCATTAACCAATACTTAAAGACAGAGTTCGATGATTTAG 1287
 DB 127 CCGAATGAGAGATCCATAGCGCGGTATTAAGAAACCTCAGTTGCGATGATCTTA 186
 QY 1288 TTCTTGAGAAACCTTCCCATTAAGTGTCTCTTAATGTTTGTAGTCCGACCTG 1347
 DB 187 TTTTGAAGAGACCTCATACCAATAGTGTCTCTTGTGATGTTTGAATCCCGGCTG 246
 QY 1348 ATGCTTGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
 DB 247 ATGCACTTGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 306
 QY 1408 GTGAGAAAGAGCTTATCAATCAACAGATATGATGATGATGATGATGATGATGATGAT 1467
 DB 307 GTGAGAAAGAGCTTATCAATCAACAGATATGATGATGATGATGATGATGATGATGAT 366
 QY 1468 CTCGTAATGTTGTGAAACCTTATGCTTCTTGTTCATCACTAAGATGATGATGATGAT 1527
 DB 367 CGGAGACTGTTGAGAGTAACTATAGACTTGTGACTTCAAGAGAGAGATCTTCTGAT 426
 QY 1528 TGCTAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
 DB 427 TGCTAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
 QY 1588 CTCGAATCAAGGCTCACTAAGATTCCTTCTTGTGAGCATGCTGATGATGATGATGATGAT 1647
 DB 487 CTCGAATCAAGGCTCACTAAGATTCCTTCTTGTGAGCATGCTGATGATGATGATGATGAT 546
 QY 1648 TATATTTGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1707
 DB 547 TATATTTGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 606
 QY 1708 CTGATTAACCAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1767
 DB 607 TGACATTAACCAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
 QY 1768 AGAGTCAAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1827
 DB 667 AGAGTCAAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726

QY 1828 GTGACCTATTGGCAGCAAGCTCTGGGATTTCCTCAAAAGCTGTTTCATTCATCAGAT 1887
 DB 727 GTGGCCCAAGAGCAAGTGCAGAAATGATATTCGGGAAACAAAATCTTTCACCAAGAT 786
 QY 1888 ATAGTTCTATGAGCTGCTGAGCTGTGATTTGATGATGATTCATGACGATTAACATA 1947
 DB 787 ACAGTTCCAGAGCTGACCGTTGAAATGATGAGAGCTATGATGATGATGATGATGAT 846
 QY 1948 TTGATCTGATGAGAGCTGATCATCATATTTGATGATGATGATGATGATGATGATGAT 2007
 DB 847 TTACCAACAGAGAGAGTGCACATGATGATGATGATGATGATGATGATGATGATGATGAT 906
 QY 2008 AGACCTTTCTAGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2067
 DB 907 AAATTTCTCTCCGCAAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
 QY 2068 CTGATGGGAGCTGTTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTT 2127
 DB 967 CTGATGGTATTTAGGTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTT 2187
 QY 2128 CCGGAGACAGTGGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2187
 DB 1027 CCGGATGCTCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
 QY 2188 GAGAGTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2242
 DB 1087 GACAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1141

RESULT 10
 ADD18749
 ID ADD18749 standard; DNA; 3256 BP.
 AC ADD18749;
 XX
 DT 15-JAN-2004 (first entry)

Human disease related protein DNA sequence SegID180.
 DE
 XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnerary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transport; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003018621-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 23-AUG-2002; 2002WO-GB003892.
 XX
 PR 23-AUG-2001; 2001GB-00020558.
 XX
 PR 05-OCT-2001; 2001GB-00024037.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 DR
 DR MPI: 2003-290046/28.
 DR P-PSDB; ADD18748.
 XX
 PT New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 XX
 PS Claim 27; SEQ ID NO 180; 424bp; English.

XX
 CC This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory, the
 CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein encoding DNA sequence of the invention.
 XX

SO Sequence 3256 BP; 828 A; 761 C; 832 G; 834 T; 0 U; 1 Other;

Query Match 13.4%; Score 341.2; DB 9; Length 3256;
 Best Local Similarity 51.6%; Pred. No. 7.4e-87;
 Matches 963; Conservative 0; Mismatches 877; Indels 27; Gaps 7;

QY 349 AAAAGCCAGATGAGTGAATGAGTGAAGAGCTTGCGCTGTTGTCAGAGTGA 408
 DB 506 AAATGCAATTCAGTCTTATGAGCAGAGCTGTGACGTCGCCGAGAGTGGCTGA 565
 QY 409 TGGCTCTTACGATATGTTGTTTAACTGATGATGATGATGATGATGATGATGATGATGAT 468
 DB 566 TGGCTCTTATGAGGCTATGTTTACCCAGTACAGATGATGATGATGATGATGATGATGATGAT 625
 QY 469 CCGACAGATTTTGAAGAACCCAAAGTCCGGAGCAACTGATGAACTGTTGATCAT 528
 DB 626 CCAATTTGATTTCCATATATGAGCAGAGCCGCCGAACTGATGAACTTATGATAC 685
 QY 529 TATTAGATCTTAAAGTTATACCAATATTTAAGAAATGATGCCATGACCTAGAAAG 588
 DB 686 TCCTTAGAATGAACATGCTCCCATTTGCAACAAATGATGATGATGATGATGATGATGATGAT 745
 QY 589 CTCATATGAGATTCATCTG-----TATATCTGGATATATGACAGTTAGAGAGC 642
 DB 746 AGCCCAAGATACCTGACAGGGGGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 805
 QY 643 TGTGGCACTGAGACGTGAAGCTGATCTCTATTTCTGCTGATGATGATGATGATGATGATGAT 702
 DB 806 GACTGGCTGTGAATGAAATGAACTGATCTTGAATGTTCTTCAATGATGATGATGATGATGAT 865
 QY 703 ATAGTGTCCACCAAGTGAACATATCAAAATGATACACTATATTAAGAAAGC 762
 DB 866 TTGACAGCCCCCAGAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 922
 QY 763 ATCAGCAAGAAATCACTTTTGGAGCAAAATCTCGTATGATGATGATGATGATGATGATGATGAT 822
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 QY 823 AAGTGAAGCTGTCTGTTGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 882
 DB 983 AGGTGAAGACACCTCTGCGCTTGGCAAGTGGACATCTGTTGATGATGATGATGATGATGATGAT 1042
 QY 883 TTGAAATCGAGCAATCTTAAGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 942
 DB 1043 CCCACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
 QY 943 AGAATGCAATTTGGGATCATCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1002
 DB 1100 GTACCTTTCTTTCAGAAATGAAGCTGACAGCCCTACTGTTGATGATGATGATGATGATGATGAT 1159
 QY 1003 CAAGAGATTTCAAGGATCTACAGAAATTTCTCATGAGAGAGCAAAAAGATATTGTC 1062
 DB 1160 CCGGATCTGAGAGAGATGTTGGCACCCTTGAACCTGAGAGAGAGAGAAATTTATCC 1219
 QY 1063 TAGATGTCAGATGCTTTGAGAGCAATGAGATTTAATAGGCTGATGAAATGAAGCTG 1122
 DB 1220 ATCATCTGCTGATCTGTTGACGAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1279

QY 1123 ATGTAGCTGGGCCCCAGTTGCTGATATGAGAGAGCTTTGGTGTCTAGATTGACTATA 1182
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QY 1240 ACCCTATTAACAGAGATCTTAAAAAGACAGAGTGTCTGATGATTTAGTTCTTGAGAAAA 1299
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QY 1300 CATCTTGCCCATTAAGTGTCTCTTAATGTTTAAAGTCCGACCTGATGCTTGTTC 1359
Db 1457 TGACTGTCCCAATGAGATTCCTGCTGATCTTTAAATCTGCTCTGCTCTTAACCC 1516
QY 1360 AGATTGATCTTTGGCAATTCGAAAGTGTATGATGCTCTCTTAAAGGTGAGAAAGAG 1419
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QY 1420 CTATCAGATCAACAGATATTCGATTAAGTTTAATCTGATGCTATCTCTGTAATGTTG 1479
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Db 1697 ACAAAATGATGATCTGATCTTCACTCCAGTGGCTCTTCCAGCTGTGCAGAGCATCCAGA 1756
QY 1600 CGTCAACTAA---GATTCCTGTCTTGGGAGTCTGATGATGATGATGATGATGATG 1656
Db 1757 AAGCTGTAAAGGAGATTCAGTATGAGGAGGAGGAGGATCTCTCAATGATATGAG 1816
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QY 2011 CTTTTCAAGCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2070
Db 2177 TCTTCTGAGCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2236
QY 2071 ATGAGGCTGTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2130
Db 2237 ATGATTAACCGCTTGGAGCTGAGAGTGAAGTGAATCAATCAATCAATCAATCAATCA 2296
QY 2131 GTGAGCAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2190
Db 2297 GGGGACAGTGAAGCTTGAAGGAGCTGCTTACTAATGATGATGATGATGATGATGATGATG 2356

QY 2191 AAGTGT 2197
Db 2357 ACGTGT 2363
RESULT 11
AAC38250
ID AAC38250 standard; DNA, 476 BP.
XX AAC38250;
AC
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 20307.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic; pathway;
KM promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
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PR 09-MAR-1999; 99US-0123548P.
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PR 17-JUN-1999; 99US-0139492P.

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PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.

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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
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PR 29-OCT-1999; 99US-0162142P.

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Query Match 12.6%; Score 321.4; DB 3; Length 476;
 Best Local Similarity 79.8%; Pred. No. 1.2e-81;
 Matches 379; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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QY 1256 ACTTAAAGACAGAGCTGATGATTTAGTTCTTGAAGAAACATCTTGGCCATTAGG 1315
DB 2 ATTGAAGACAGAGCTGATGATTTAGTTCTTGAAGAAACATTTGCCATTGGG 61
QY 1316 TGTTCCTTAATTGTTTGAATCCCGACCTGATGCTTGGTTCGATTCATCTTGGC 1375
DB 62 TGTTCCTCAATTATTTTGAATCTGCTTCCTGATTCGATTCGATTCGATTCGATTCG 121

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Db 549 TCACTTTGTATGGTGG 564

RESULT 13

ID AAC78003 standard; cDNA; 2507 BP.

AAC78003;

DT 08-FEB-2001 (first entry)

DE	Human cancer associated gene sequence SEQ ID NO:397.
yy	

KW Human cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
 KW antidiabetic; antistatic; antineumatic; antiarthritic; antiviral;
 KW antinflammatory; antihypoid; antiallergic; antibacterial; cardiac;
 KW dermatology; neuroprotective; thrombolytic; coagulant; nootropic;
 KW vasotrophic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haemotopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening; ss.

OS Homo sapiens.

PN WO200055350-A1
XX

PD 21-SEP-2000.
YY

PF 08-MAR-2000; 2000WO-US005882.
XY

PR 12-MAR-1999; 99US-0124270P.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX

PI rosen CA, ruben SM,
XX

DR WP1; 2000-587533/55.
DR P-PSDB: AAB43794.

XX PT	Novel isolated m
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XX FI useful for clearing or diagnosing e.g. cancer.

ES Cialini, Page 370; English
XX

CC AACT7667 to AAC8448 encode the human cancer associated proteins given
CC AAC7398 to AAC8429. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerability; immunomodulatory;
CC antidiabetic; antischismatic; antineumatic; antiarthritic;
CC antiinflammatory; antihypoid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
CC neurologic; vasotropic; antiparasitic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of hematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC7849 to
CC AAC8457 and AAC8420 represent sequences used in the exemplification of
CC the present invention

Sequence 2507 BP; 667 A; 566 C; 621 G; 645 T; 0 U; 8 Other;

Query Match	10.9%	Score 278.2;	DB 3;	Length 2507;
Best Local Similarity	51.6%	Pred. No. 8.9e-69;		
Matches 813; Conservative	1;	Mismatches 739;	Indels 22;	Gaps 74

QY	636	GCAGGACGTGTGGACATCGGAACCGAAAGCGATCTCCTTATCTGCGTCAAGTATGTGAAAT	695
Db	2	GCCTCCGCACTGCCTGTGGAAATGAAATCGATCTCTGATATGTTCTTTCAAGATGTAGAA	61
QY	696	GGGTGTATATAGTGTCCACAGTGAACATCATCAAAATTCATACACTTATATTTAA	755
Db	62	GGCCTTTTATACAGCCCCCAGGTTCCAGATGATGCAAAAGTTTATGTAATTTATCC	121
QY	756	GAAAGCATCAGCAAGAAATCATTTTGGACAAATCTCGTATAGGTAAAGAGCATG	815
Db	122	GGAGATGACAGACTGT---TGACATTTGAAACCAAGCTTAGAGTGGAAATGGGTGGCATG	178
QY	816	ACAGCAAAAGTGAAGGCTGCTGTCTTGGCTTCAAATATGCGGCACACTGTGTATTTACA	875
Db	179	GAACCCAAAGTGAAAGCAGCCCTCTGGGCTTTGCAGGTGGCACTTCTGTGTGWTATGCC	238
QY	876	AGTGGCTTTGAAATCGAGACATTCCTTAAAGTCTTTCATGGGAAAAAATTGGTACTCTC	935
Db	239	AATGAAACCCACCAAGATGTCTGGGCACTCATCAACATGTGGAGGGGAAGAA	298
QY	936	TTTACAGAAATGCGAATTTGTGGGAATCATCTTAAGATGTAGTACTCGTGAATGGCT	995
Db	299	GTT---GGTACCTTCTTTGAAAGTAAAGCTTCGACGGCTTACTGTGTGACGACGGGA	355
QY	996	GTTGCCCAAGAGATTTGTTCAAGGCATCTACAGATTTGTTCATCAGAGAACAAAAAG	1055
Db	356	GAATGTGGCGGATGTGGAGGAAGATTTGGCCACTTGGAACTGTGACAGAGAGCAGAA	415
QY	1056	ATATTGCTAAGATTTTGCAGATGCTTTGGAGGCAATATAGATTTTAAATTAAGTGTGAAT	1115
Db	416	ATTATTCATCATCTCGGTGATCTGTGTACGACACAGCGTATGATGATCTGTTAGCCAC	475
QY	1116	GAACCTGATGATGCTGGCGCCCAAGTTCAGATATGAGAAGCCTTTGGTGTCAATG	1175
Db	476	AAAAAAGCTTGGAGGAGGC---AGAGGGAGACTTGCAGTCTCTGTGAACGTTTA	532
QY	1176	ACTTATAAACCCAGAAAGATATGCAAGCTTGCATAATCTATGTS---TACCCTTGCAAT	1232
Db	533	AGCCTTCATCATCAATTAATGAAACAGCTTGCCCATCGGTGCGACAGATGTGCAAGCTCC	592
QY	1233	ATGGAAGCCCTATAAACCAAGATCTTATAAAAGACAGAGGTGCTGATGATAGTTCTT	1292
Db	593	TCCACAGACACAGCGGGAGCGTGTTTGGCGCGCACCGAAATCGCAAAAATTGGAATCG	652
QY	1293	GAGAAACATTTTGGCCATTAGTGTTCTCTTAATTTGTTTGTGCCACCTGAATGCC	1352
Db	653	GAACAAGTACGTCTCCCAATTGGAGTTCTGTGTGATCTTTGAATCTCGTCTGACTGT	712
QY	1353	TTGGTTCAATGTGATCTTTGGCAATTCGAAGTGTATGTCTTCTCTTAAAGTGA	1412
Db	713	CTACCCGAGGTGGCAGCTTTGGTATGCAAGTGGCAATGGCTTTTAACTCAAAAGAGGG	772
QY	1413	AAAGAAAGTATCAATCAACACAGATATGTAGTAAAGTTTAACTGATGCAATCCCGT	1472
Db	773	AAGAGGTGTCACACAGCACCGGATTTCTCACTCTTGACCCAGAGGCTCTCTCAATC	832
QY	1473	AATGTGTGAAAACTTATTTGGCCTTGTTCACACTAGAGTGAATGCAATTTGCTA	1532
Db	833	CATGAGTCAAGAGAGCGCGTCAACTGGTGAATCCAGAGAAAGATGAAAGATCTTTCG	892
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Db	893	CGCTTAGCAAAATGATGATCTATCATCTTCCAGTGTCTTCCGACGTGTCAAGAC	952
QY	1593	ATCAAGCGCTCACTAA---GATTCCTGTCTTGGCATGCTGATGTATATG---CCAGCT	1648
Db	953	ATCCGAAGCTGTCTTAAGGGATTCAGATGATGGGGCACAGCGAAGGATCTGTGCATAT	1012
QY	1649	ATAATTATACAATCAGCTGACATGATATGACAAAATCTTATTTAATGATGCAAAAAC	1708
Db	1013	GTAATGTGATTCGAGGCGCAGGTGTGAATAGGTCAACAGGCTATGACGAGACTTAAATG	1072

1203 CT---TGCAAAATCTATTCGTACCTTGCATATATGAGAACCTTAAACAGATATCT 1259
 Db CTCCTCCCTGCGCCGGAAGCAATCCGAGAGACATGACAAAGATGTGGCTGTCTCG 1449
 Qy 1260 AAAAAGACAGAGTGTCTGATGATTTAGTTTGTGAGAAAACATCTTCCCATTAAGTGT 1319
 Db 1450 AGACGCAACCCGCTTGGGAGATCAGCTGAGCTCAAGAGAGGTCACTGTGCCATAGGCGTC 1509
 Qy 1320 CTCTTAATGTTTGTGATCCCGACCTGATGCCCTGGTTCAGATGATGATCTTGGCAATT 1379
 Db 1510 CTACTGCTATCTTCGATCCCGCCGACATCTGCTGCTTAAGTGGCCGCTTGGCAATG 1569
 Qy 1380 CGAAGTGTATGCTCTTCTCTTAAAGGTGAGAAAAGAGCTATCAGATCAACAGATA 1439
 Db 1570 GCTCGGCAACGAGACTGCTCTCAAGGGGGGCAAGAGCGGCAACAGCAACAAGGCC 1629
 Qy 1440 TTGATAGATTAATGATGATGATCTCTCTGATGATGATGATGATGATGATGATGAT 1499
 Db 1630 CTATGAGCTGTGCAAGAGAGGCGCTGCGACCGTGGAGCGAGGACGCGCTGTCACTG 1689
 Qy 1500 GTTACAACTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1559
 Db 1690 GTTTCACGCGCGGAGAGATCAGGATCTGCTGCTCAATGAGAACACATGACCTGATC 1749
 Qy 1560 ACTCCAAAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1616
 Db 1750 ATTCGCGCGGCTCTCTCGACCTGATGCGAGCATCCAGAGAGATGCTGACATCC 1809
 Qy 1617 GTTCTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1676
 Db 1810 GTGCTGGGCGACGCGAGAGGCTGTGCACTCTCAATGACAGAGATGAGATCTGAG 1869
 Qy 1677 ATGCAAAACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1736
 Db 1870 AAGCCCTGCGCATGTCACGCGAGCGCAAGTCCATTAATCCGCTGCTTCAACGCGCATG 1829
 Qy 1737 GAGACCTTACTAGTTCATTAAGATCTTAAGAGATCAAGGCGCTGACGACATATTAGTA 1796
 Db 1930 GAGACCTGCTGATTCACAGAGACCTGATGATGATGATGATGATGATGATGATGAT 1989
 Qy 1797 GCACATAAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1856
 Db 1990 ATGCTGAACGTGAGGGGCGTCATAATCTATCCGACCGCGCTGAACACAGACCTGACA 2049
 Qy 1857 TTT-----CGAAAGCTGTTTCAATTCATGATGATGATGATGATGATGATGATGAT 1910
 Db 2050 TTTGCG 2109
 Qy 1911 GAGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1970
 Db 2110 GAGGTTGCGCGAGCTGAGAGAGGCGCATTAATCAATCCATGATGATGATGATGATGAT 2169
 Qy 1971 ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2030
 Db 2170 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2229
 Qy 2031 AGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2090
 Db 2230 AGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2289
 Qy 2091 GGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2150
 Db 2230 GGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2289
 Qy 2151 GGTCTCTTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2193
 Db 2330 GGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2392

RESULT 15
 ABA90521_16/c
 Continuation (17 of 24) of ABA90521 from base 1600001 (Genomic sequence of Lactococcus)

WP	Sequence split into 24 fragments	LOCUS ABA90521	Accession ABA90521
WP	Fragment Name	Begin	End
WP	ABA90521_00	1	110000
WP	ABA90521_01	100001	210000
WP	ABA90521_02	200001	310000
WP	ABA90521_03	300001	410000
WP	ABA90521_04	400001	510000
WP	ABA90521_05	500001	610000
WP	ABA90521_06	600001	710000
WP	ABA90521_07	700001	810000
WP	ABA90521_08	800001	910000
WP	ABA90521_09	900001	1010000
WP	ABA90521_10	1000001	1110000
WP	ABA90521_11	1100001	1210000
WP	ABA90521_12	1200001	1310000
WP	ABA90521_13	1300001	1410000
WP	ABA90521_14	1400001	1510000
WP	ABA90521_15	1500001	1610000
WP	ABA90521_16	1600001	1710000
WP	ABA90521_17	1700001	1810000
WP	ABA90521_18	1800001	1910000
WP	ABA90521_19	1900001	2010000
WP	ABA90521_20	2000001	2110000
WP	ABA90521_21	2100001	2210000
WP	ABA90521_22	2200001	2310000
WP	ABA90521_23	2300001	2365589

Query Match	Best Local Similarity	Score	DB	Length
376 AGCTTTGCGCGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	9.6%	245.4	DB 6	110000
52451 AGCTTTGCGCTTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	48.4%	Pred. No. 2.3e-58		
Matches 892; Conservative	0	Mismatches 911	Indels 40	Gaps 6
52391 GTTATTCGCAAAAGTTTCTAGTATCTTTCAGATGATGATGATGATGATGATGATGATGAT				
496 TCGGGAGCACTCACTGAACTGTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT				
52331 GTGCTGAGAT				
556 TTAATGAAATGAT				
52271 TTAATGAAATGAT				
616 TCTGGATTAATGAT				
52220 TTGCTGATTAATGAT				
676 TTCTGCTCAGTATGAT				
52160 TTAATGAT				
736 TCAATACACTTAAT				
52100 AAATTTTAAT				
790 AATCTGCTAGTATGAT				
52040 GTTCCGCTTTTGGAACTGCGGAGAT				
850 ATAGCGGCAACCTGCTGATTAAT				
51980 AAATATGTCMAAAATGAT				
910 TTCTATGAGGAGAAATTTGAT				
51920 TCGAAGAGAT				
970 AGAT				

Db 51862 AGCATGATTTGAAGACTTGATTTAAAGTTAAAAAGCGAGCAAGAG-----TAGCA 51808
 Qy 1030 ATTTGTCATCAGAGGACGAAAAAGATTTGCTGATGTTGCAAGTGGTTGGAGCA 1085
 Db 51807 AGCTATCACTGCCGCAAAAAAGTTTGTGCAAAATTTAGCTGACAGCTTATCGAA 51748
 Qy 1090 ATGAGATTTAATAGATCTGAGATGAGAGTATGATGCTGAGGCGCCAGTTGCTGAT 1149
 Db 51747 ATACTGACAGAAATTTATTTCTGAGAAATGAAAAAGATTTGGCTTAACGCTCGAACAATGGA 51688
 Qy 1150 ATGAGAGCCTTTGTTGCTGATGATGATGATTAACAGAAAGATGAGACGCTTGCA 1209
 Db 51687 TTTCTGAGATTTAGATGACCGCTTGCCTAAATCGCAAGAAATTTCTGATATGCA 51628
 Qy 1210 AATCTTTGCTACCTTGCAAAATAGAGAGACCTTAACAGATTAATAAAGACAG 1269
 Db 51627 CAGGATGAGACAGTTGCAAACTTCTGACCCAAATAGGCAATTTGCAAGGTTCA 51568
 Qy 1270 AGGTGCTGATGATTTAGTCTTGAGAAAAATCTTCCCATTAAGTGTCTCTTAATG 1329
 Db 51567 CTATCTGATGACTTAAGATTTTGCAAAAAAGATGCACTTGCACTTTGGAATGA 51508
 Qy 1330 TTTTGAATCCGACCTGATGCTTGGTTCAATGCACTTTGGCAATTCGAAGTGTA 1389
 Db 51507 TTTTGAAGTCGTCAAATGATGATGATGCTTTTCTCTTGTTTAAACAGGA 51448
 Qy 1390 ATGCTCTTCTCTAAAGGTGAAAGAAAGCTATCATCAACACGATATTGCAATAG 1449
 Db 51447 ATTCGTTTGTATGCGGAGGAGCTGAGCGCAATTTATTAATGTTTATGTTGAA 51388
 Qy 1450 TTATTAATGATGCTATTC-----CTCGTAATGTTGGTGAATACTTAATGGCTTG 1500
 Db 51387 TTATTAAGAAAAATTTGCTGTCAGCAAAAAATTTACTGACGAGAGCTGAATTTATCTG 51328
 Qy 1501 TTACACTGAGATGATGATGAGATTTGCTAAAGCTGATGATGATGATGATGATGATG 1560
 Db 51327 ACACAGTCATGCTGAAAGCAAAAAATGAGAGAGATTAATTTTATGATGTTTGA 51268
 Qy 1561 CTCGAGAGAGATTAATTAAGCTTGTCTCTCAATCAAGGCTCACTTAAGTTCTGTTTC 1620
 Db 51267 TTCGAGAGGATGAGGCGATGATTAACGCTGCAAAAGAAAAAGCAAGGTTCTGTC 51208
 Qy 1621 TTGGGAGCTGCTGATGATGATGAGATTAATTAATTAATTAATTAATTAATTAATTA 1680
 Db 51207 TTGAACTGGGAGGATTAATTAATTAATTTTGTATGATGATGCTGATTTAGAAATG 51148
 Qy 1681 CAAAACTTATTAATGATGATGATGATTAATTAATTAATTAATTAATTAATTAATTA 1740
 Db 51147 CGACAAAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 51088
 Qy 1741 CTTTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
 Db 51087 GTTTAGGATGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 51028
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 Db 51027 ATTAAGTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 50968
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 Db 50967 GAATTCCTGCAACTGAGATGATTTTGGACAGAAATTTTATTAATTAATTAATTA 50908
 Qy 1912 AGTTGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1971
 Db 50907 AAACGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 50848
 Qy 1972 CAGATTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2031
 Db 50847 CAGAAAGCATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 50788
 Qy 2032 GTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2091
 Db 50787 CGGAGCGGTTATGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 50728

Qy 2092 GTGCTGAGTTGGCATTAAGACAGAGGCGTATTCATGCGCCGTGGACCAAGTGGTGAAG 2151
 Db 50727 GTGCTGAAATTTGGCATTTCAATCTCAAAAACTTCAATGCTCAAGAGGCAATGGCTTAAGAG 50668
 Qy 2152 GTCTTTAATTAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2194
 Db 50667 CTCTAACCTCAACAAAAATATCTGATGATGATGATGATGATGATGATGATGATGAT 50625

Search completed: March 10, 2004, 11:20:21
 Job time : 890.685 secs

Db 2074 TGGCGTGTGTTTCATTAAGCAGCAAGGTTCTGTGACGGAGCGCTTTGGGTTAGG 2133
Qy 2093 TGGTGAAGTTGGCATAAGCAAGAGCGGTATTCATGCGCGGTGAGCAAGAGGTTGAAGG 2152
Db 2134 TGCAGAGGTTGGCATTAAGTACAGGCGCATATGCGCGGAGCTGTGTGAGTTGATGG 2193
Qy 2153 TGTCTTAAGTACAGTATGATCTTGGAGAGAGCGTGGCAAGTGTGAAATGAGTGAAGAGA 2212
Db 2194 ACTTCTTAAGTACAGTATGATCTTGGAGAGAGCGTGGCAAGTGTGAAATGAGTGAAGAGA 2253
Qy 2213 TGTGTGATACACCATTAAGAGTCTTCTTGTGCAATGAGTCAATGCTCTTTT 2266
Db 2254 AGTGTGTTACACCATTAAGAGTCTTCTTGTGCAATGAGTCAATGCTCTTTT 2307

RESULT 2
AY109740 1961 bp mRNA linear HTC 17-OCT-2002
LOCUS AY109740
DEFINITION Zea mays CL2942_1 mRNA sequence.
ACCESSION AY109740
VERSION AY109740.1 GI:21213575
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1961)
Kainer, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteitt, M.S.,
Arthur, L.W., Hanley, M., Morgan, M. and Tingey, S.V.
Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 1961)
Coe, E.H.
JOURNAL Direct Submission
AUTHORS Submitted (25-APR-2002) Maize Mapping Project, University of
TITLE Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
these are publicly available from ZMD and may be found by BLAST
searching at MSU, maize.msu.edu; ZMD, www.zmd.iaate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schabale, Iowa State, then clones may be requested from ZMD:
www.zmd.iaate.edu.

FEATURES
source Location/Qualifiers
1. 1961
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/Dupont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN
Query Match 45.6%; Score 1167; DB 11; Length 1961;
Best Local Similarity 81.5%; Pred. No. 5.1e-250;
Matches 1309; Conservative 0; Mismatches 297; Indels 0; Gaps 0;

Qy 647 GGCACTGGAAGTAAAGCTGATCTCTTATCTGCTCAAGTATGATGGTGGTTATAG 706
Db 2 GGCAAGGAGGACTTAAGCAGATCTCTTGTCTAAGATGATGATGCTCTATACG 61
Qy 707 TGTGTCACCAAGAGCAATCAATCAAAATCAATACACTTATATTAAGAAAGATCA 766
Db 62 CGGTCCACCAAGCAACCGGATCAAAAGATCAATCAATCAATCAAAAGATCAATTA 121

Qy 767 GCAAGAAATCACTTTTGAAGCAAAATCTGTTAGTGAAGAGGCAATGACCAAGAAAGT 826
Db 122 CAGTGAATATACCTTTTGGGATTAAGTCAAGTGAAGAGGAGATGACACTAAAGT 181
Qy 827 GAAGGCTGCTGCTTGGCTTCAAAATAGCGGCAACCTGTGGTATTATCAAGTGGGTTGA 886
Db 182 GAAGGCTGCTTGGCTTGGCTTGAAGAGTGGCAACCTGTGGTATTATCAAGTGGGTTGA 241
Qy 887 AAATGAGCAATCTTAAGTCTTCAATGGGAAAAAATGTTACTCTCTTCAAGAA 946
Db 242 ATCTCAAGCAATCTTGAAGTCTTCAAGAGAGAAATGTTACTCTCTTCAAGAA 301
Qy 947 TGGCAATTTGGGAAATCACTAAGATGTTAGTCTGAGATGGCTGTGGCGGAG 1006
Db 302 TGCAGATCTGAGAGCAATCAAGATGTTAGTCTGAGATGGCTGTGGCGGAG 361
Qy 1007 AGATTGTTCAAGGATCTAAGAAATTTGTATCAAGAGAAAGAAAGATTTGTCTAGA 1066
Db 362 AGAATGTTCAAGGCTGTGAGAAATTTATCATGAGATGAACGAAAGAAATTTGTAGA 421
Qy 1067 TGTGCAATGCTTTTGAAGCAATGAGATTTATTAAGTCTGAGATGAACCTGATGT 1126
Db 422 CATTGAGATGCTTTTGAAGCAATGAGATTTATTAAGTCTGAGATGAACCTGATGT 1186
Qy 1127 AGTGGCGCCCAAGTCTGAGATGAAGAGCTTTGTTGCTAGATGCTAATAAC 1186
Db 482 NNN 541
Qy 1187 AGAAGATGAGCAAGCTTGCAGAAATCTTGTACCTTGCAGAAATGAGAGAGCTGAT 1246
Db 542 AGAAGATGAGCAAGCTTGCAGAAATCTTGTACCTTGCAGAAATGAGAGAGCTGAT 601
Qy 1247 AAACAGATCTTAAGAAAGAGAGGTTGCTGATGATTTAGTTCTTGAAGAAACATCTT 1306
Db 602 CAACCAATCTTAAGAAAGAGAGGTTGCTGATGATTTAGTTCTTGAAGAAACATCTT 1366
Qy 1307 CCATTAAGTGTCTTAAATGTTTGAAGTCCGAGCTGATGCTTGTGATGATGCT 1426
Db 662 CCCTGAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 721
Qy 1367 ATCTTGGCAATGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1426
Db 722 GTCTTGGCAATGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 781
Qy 1427 ATCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1486
Db 782 ATCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 841
Qy 1487 ACTTATGAGCTTGTCACTAGATGATGATGATGATGATGATGATGATGATGATGAT 1546
Db 842 NCTTATGAGCTTGTCACTAGATGATGATGATGATGATGATGATGATGATGATGAT 901
Qy 1547 CATTGATCTGTCACTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606
Db 902 CATTGATCTGTCACTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 961
Qy 1607 TAAATCTGCTTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1666
Db 962 TAAATCTGCTTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021
Qy 1667 TGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1726
Db 1022 TGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1081
Qy 1727 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1786
Db 1082 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1141
Qy 1787 CATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1846
Db 1142 TATCTCTATCACTCAAAAGAGAGGTTGCTATTTATGAGAGGCTGTGCAATGA 1201

[illegible]

	RESULT 3	
AY105865		
LOCUS		
DEFINITION	Zea mays PC0085448 mRNA sequence.	1685 bp linear HTC 16-OCT-2002

KEYWORDS	HTC.
SOURCE	Zea mays
ORGANISM	Zea mays

REFERENCE
1 (bases 1 to 1685)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.

TITLE	AUTHORS
Maize Mapping Project/Dupont Consensus Sequences for Design of	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitstett,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.

JOURNAL
OF
OVERGRO
UNPUBLISHED (2002)
2 (baes 1 to 1685)

AUTHORS Coe, E. H.
TITLE Direct Submision
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,

FEATURES
source
1. 1685
location/Qualifiers

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/organism="Zea mays"
/mol_type="rRNA"
/db_xref="MaizEDB:63479"
/db_xref="raxon:457"
/clone_id="Maize Mapping Project/DuPont Cornsensus
library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
configs to seed DuPont configs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

```

ORIGIN

Query Match	35.0%	Score 891.6;	DB 11;	Length 1685;
Beet Local Similarity	77.5%;	Pred. No. 7.86-220;		
Matches 1080;	Conservative	0;	Mismatches 314;	Indels 0;
			Gaps	0

OY	906	GTTCCTTCATGCGGAAAAAATTTGTA	CTCTCTTTTCACAGAAATCGCAATTTG	GGGAACTCA	965	
Dp	11	GTTCCTCAAGGCGGAAAAATCGTA	CACTTTCCACACAGCAAAATTTG	GGGCAATGT	70	
OY	966	TCTAAGAGATGTAGTACTCGTAGA	TGGCTGTGGCCCAAGAAATTTCA	AGGCATCTA	1021	
Dp	71	TCCAAAGAGACTACAGCCCGAGAG	TGGCAAGTTGCGCAGAGACTGTTC	AGGCGCTCTA	130	
OY	1026	CAGAAATTTGTCA	TGAGAGAAACGAAAAAGATAT	TGCTAATGTTCCAGATGCTTTGGAG	1085	
Dp	131	CAGAAATTTGTCA	TGAGAGAAACGAAAAAGATAT	TGCTAATGTTCCAGATGCTTTGGAG	190	
OY	1086	GCAAAATGAGAGATTTATATAG	TTAGGTTGAGAAATGAACTGATGAC	TGACCTGCGGCCCAAGTTGCT	1144	
Dp	191	GCAAAATGAGAGATTTATGAT	TGCTGAAATATGATCCGATGTTGAG	CAGACAAAGTTGCT	250	
OY	1146	GGATATGAGAACCTTTGGTGTCT	GTCTGATGACTTTAAACCAAGAAAGAT	AGCAACCTT	1205	
Dp	251	GGTATGAGAAATGCTGTGTTGCT	GTGAGATGACCTTAAGCCAGAAAGAT	TACAAATCTT	310	
OY	1206	GCAAAATCATTTCTGTACCTT	GCAAAATATGAGAAACCTTTAAAC	CAGATACTTTAAAG	1265	
Dp	311	GCAAGATCATTTCTGTAAAC	TGCTGACATGAGAGACCTTATTTCC	CACTATGAAAGA	370	
OY	1266	ACAGAGTTGCTGATGATTTAG	TTAGTTCTTGAGAAACATCTTGCCCAT	TAGTGTCTCTTA	1322	
Dp	371	ACAGAGTTGCTGAAAGATCTG	ATTTTGAAGAACATATGCCCCAT	TGGTGTCTTCTC	430	
OY	1326	ATGTTTTGAGTCCCGACCTG	ATGACCTTGTTGATTCAGATTC	CTTTGGCAATTCGAGT	1385	
Dp	431	ATATTTTTGAGTCTCGTCTG	ATGACATTTGCTCAGATTCATCTC	TACGACATCCGAGT	490	
OY	1386	GGTAATGCTCTCTCTTA	AAAGGTGGAANAAGACTTCA	GATCAACCGAATATGAT	1445	
Dp	491	GGTAATGCTCTCTTTGA	AAAGGAGGAAAGATTTATGAG	ATCOAAATATATATAC	550	
OY	1446	AAGGTATTAACGATGCTAT	TCTCGTATATGTTGGTAA	AAACCTTATTTGGCCTGTTACA	1505	
Dp	551	AAGGTATTAACGATGCTAT	TCTCGTATATGTTGGTAA	AAACCTTATTTGGCCTGTTACA	610	
OY	1506	ACTAAGAGATGATCGCA	TTTGGTAAAGTTGATATGATCA	TATGATCTGTGCACTCA	156	
Dp	611	AGCAAAAGAGAAATGCTG	ATCTATACGCTTATATGATTA	TGATCTGTGCACTCCG	670	
OY	1566	AGAGAGATTAATAGCTGT	CTCTCAATCAAGGCGTCA	CTAAGATTTCTGTTCTGG3	162	
Dp	671	AGAGAGATTAATGCTGT	CTCTCAATCAAGGCGTCA	CTAAGATTTCTGTTCTGG3	730	
OY	1626	CAGCTGATGATATATG	CCAGTATATTTGACAAATCAG	TGACATGATATGAGCAAAA	168	
Dp	731	CAGCTGATGATATCTG	CCATGTTTCACTTACAAATCAG	CCGACATGATATGAGCAAAA	790	
OY	1686	CTTATTTGATGATGCA	AAAACTGATTTCCACAGACCT	CTGCAATGATGAGACTTTA	174	
Dp	791	CGGATGATTTGATGATG	CTAATGATTTATCCACAGATG	ATATGAAATGAGAAACCTA	850	
OY	1746	CTTAGTTCA	TAAAGATCTTTATGAAAGTCCAG	CGCTTGACGCAATATATAG	AGCACTAAAA	180
Dp	851	CTTAGTTCA	TAAAGATCTTTATGAAAGTCCAG	CGCTTGACGCAATATATAG	AGCACTAAAA	910
OY	1806	ACAGAGAGATTAATAT	TTATTTGATGAGACTTATGCGCA	CAAAGCTCTGGATTTCCAAA	186	
Dp	911	AAAGAAAGAGATGATTA	TTATTTGATGAGACTTATGCGCA	CAAAGCTCTGGATTTCCAAA	970	
OY	1866	GCCTTTCA	TTCATCATGATGATATGTTCT	TATGAGCTGACGCTGTGATGTTGATAT	1921	
Dp	971	GTAAGCTACTTTCG	TCAATGATATGCTCAATG	CGCATGCAACAGTCTGATTTGTTGAT	103	

Qy	1926	GTTCAATGACGAATTGACCAATTCATGCTATGGAAGTGCCTAACAAGATTGATGCTC	1985
Db	1031	GTCGAGTAGCTATGCAATGCACTAAATGCTTATGGAAGTGCACACACAGACTGCATATC	1090
Qy	1986	ACTACAGATGATTAAGGTAGCAGAGACTTTCTACGACAGATTGATAGTGCCTGTAATT	2045
Db	1091	ACAACGTGTAGAAGTGTGCAGAGGCCCTTCTGTGCAGCAAGTTGATAGTGCCTGTGTTT	1150
Qy	2046	CATAATGCAATGACGAGATCTCTGATGGGGCTGTTTGATATTGGGCTGAGAGTTGCC	2105
Db	1151	CATATGTCAGACACAGGATTTTGATGAGGACGCGTTTGAGCTAGAGTGCTGAGGTTGGC	1210
Qy	2106	ATAAGCACAGGAGCGCATCATGCCCCGTGACACAGTGGGTGTTGAAGTCTCTTAATACA	2165
Db	1211	ATAAGTACAGAGCGGATACATGCCCCGGAGCTGTGGAAGTTGATGACCTTCTAACTACT	1270
Qy	2166	CGATGGAATCTTTCGAGAGCGTGGGCAAGTGTGTAATGGTGAACAAGATGTGCTGTACCC	2225
Db	1271	CGCTGCATTTTGGCGGGTAGTGGACAAGTGGTAATGGTGAACAAGGAGTGGTTTACACC	1330
Qy	2226	CATAAGAGTCTTTCCTTTGCAATGAGGTCAAAATGCTCCTTTTAACTGTTCAGAGTAGGT	2285
Db	1331	CACAAAGATCTTCTCTTTGCAATGAGGCCAAATACCTCGCTGTGGTGTGTAACGAATGGCT	1390
Qy	2286	GAATATCCTTTTAA 2239	
Db	1391	GGAATCCCCCTTTTA 1404	

RESULT 4	CD893850	787 bp	mRNA	1 linear	EST 14-UTL-2003
LOCUS	G118.124L04F010828	G118	Triticum aestivum	CDNA clone	G118124L04
DEFINITION	CD893850 G118.124L04F010828 G118 Triticum aestivum mRNA sequence.				
ACCESSION	CD893850				
VERSION	CD893850.1	GI:32664761			
KEYWORDS	EST.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 787)		Genoplate, a major partnership french program in plant genomics		
		Genoplate, a major partnership french program in plant genomics		
		Unpublished (2003)		
		Contact: Genoplate		

93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the French
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.inbiohogen.fr>).

FEATURES	Location/Qualifiers
source	1. .787

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/organism="Triticum aestivum"
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pollination)"
/clone_11b="G118"

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Query Match	22.6%;	Score 575.2;	DB 14;	Length 787;
Best Local Similarity	84.7%;	Pred. No. 8.1e-138;		
Matches 657; Conservative	0;	Mismatches 118;	Indels 1;	Gaps 1

563 AATGATGCCATCAGCAGCTGAAAGGCTCATATAGGATTCATCTGTATATTCTGGGA 622

Db	12	AAATGATGCCATCGATGACGAAAGAGCGCTCCATACGAGGATTCATCTGGTATATATCTGGGA	71
QY	623	TAAAGACAGCTTACGAGACGCTGTGCGACCTGGAACCTGAAACCTGATATCCCTATATCTGCT	682
Db	72	TAAAGACAGCTTGGAGAGGCTTACTGCGCACTTGGAACCTGAAAGCTGATCTCTGTGCTCT	131
QY	683	CAGTATGTGATGGGTGTATAGTGTGTCCACCAAGTGAACCATCATCAAAATCATACA	742
Db	132	TAGTGAATGTGATGGCTCTACAGGGGCTCCACCAAGTGAACCTTCATCAAGTTATATACA	191
QY	743	CACCTATATTAAAGAAAGCATCGACGAAGATCACTTTTGAGAGCAATCTCGTGTAG	802
Db	192	TACTTATATCAAGAAACATATATCAAGAAATTACTTTGAGCAAGTCCCGGTGG	251
QY	803	TAGAGGAGCATGACAGCAAAAGTGAAGGCTGCTGTCTTGCTTCAAATAGCGCACACC	862
Db	252	TAGAGGTGGCATGACAGTAAAGTCCAAAGTGCCTGTGTGGGCTTCAAGGGGTGTATGC	311
QY	863	TGTGTTATTACAAGTGGCTTGAAGATCGAGCATTTTAAAGTTCTTCAATGGGGA	922
Db	312	TGTTGTATTACAAGTGAATGTGATCTCAAGCGCTGTGTTAAAGTTCTCGGTGGGA	371
QY	923	AATGTTACTCTCTTCAACAAGATGCGAATTTGNGGATCATCTAAGATGTTAGTAC	982
Db	372	AATGTTACTCTTTTCAATAAATGCAAGTTGTGTGGAACCATCCAGACACCAAGGT	431
QY	983	TCTGTAGATGCGCTGTGCGCAGAGATGTTTCAAGGCATCTACGAATTTGTCTACA	1042
Db	432	CCGTGAATATGCTGTGTGTCGACCGGATGTGTTCAAGGGTCTCAAGATTTGACATCGA	491
QY	1043	GGAACGAAAAAGATATTTGTAGATGTGCGAGATGCTTTGAGGCAAAATGAGATTAT	1102
Db	492	GGAAGCGAAGAAATTTAGTATGATGTGCGGATGCTTTAGAGCAAAATGAGATTAT	551
QY	1103	AAGGCTTGAGATGAAGCTGATAGTGTGCGGCCCAAGTTGCTGATATGGAAGCTTT	1162
Db	552	TAGATCCGAGATGAAGCAGATTTAGACAGCAGCAATGAGGCTGGTATGAGAGGCTTT	611
QY	1163	GGTTCATGATGCTATTAACACGAGAAAGATGACAAAGCTTGCAAAATCTATCTGATC	1222
Db	612	GGTTTCTAGATTGCTCTGAACCAAGAAAGATGCAAGCTTGCCAAATCTGTTCGCAC	671
QY	1223	CTTTCGAATATGAGAGACCTATTAACCAAGATCTTAAAAAGACAGAGGTTGCTGATGA	1282
Db	672	TCTTCGCAATATGAGAGACCTATTAACGAGATCTGAAAAAGACAGAGGTTGCTGATGG	731
QY	1283	TTTAGTTCTTGAAGAAACATCTTGCCCATTTAGTGTCTCTTAAATGCTTTTAG	1337
Db	732	TTTAGTTCTTGAAGAAACATCTTGCCCTTGGGGTGTCTTAATGATTAATTTGAG	787

RESULT 5	CD869253	698 bp	mRNA	linear	EST 11-JUL-2003
LOCUS	AZ02	TttrfCum	aestivum	CDNA clone	AZ02111C08,
DEFINITION	mRNA sequence.				

ACCESSION CD869253
 VERSION CD869253.1 GI:3253069
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

EST.
 Triticum aestivum (bread wheat)
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 698)
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.inbio.gen.fr>.

FEATURES

source

1..698
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ORIGIN

Query Match 22.1%; Score 563.6; DB 14; Length 698;
Best Local Similarity 88.0%; Pred. No. 7.9e-135;
Matches 614; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

1127 AGCTGGGCCCCAGTGTGCTGATATGAGAGACCTTTGGTCTGATGATTAATAAAC 1186
1 AGCAGCAGCAGTATGAGCTGGGTATGAGAGCTTTGGTCTGATGATTAATAAAC 60

1187 AGAAGATAGACAGCTTGCATAATCTGATCTGCAATATGAGAGACCTTAT 1246

61 AGAAGATAGACAGCTTGCATAATCTGATCTGCAATATGAGAGACCTTAT 120

1247 AAACAGATCTTAAAGACAGAGCTGCTGATGATTAAGTCTTGAAGAGACCTT 1306

121 TACTAGATCTGAAAGAGAGAGCTGCTGATGATTAAGTCTTGAAGAGACCTT 180

1307 CCCATTAAGTGTCTTATTTTGTGAGTCCGACCTGATGCTTGTGATGATG 1366

181 CCCATTAAGTGTCTTATTTTGTGAGTCCGACCTGATGCTTGTGATGATG 240

1367 ATCTTGGCAATGCAAGTGTGATGCTTCTCTTAAAGTGTGAAAGAGATCAG 1426

241 GCTTTAGCCATCGAAGTGTGATGCTTCTCTTAAAGTGTGAAAGAGATCAG 300

1427 ATCAACAGCATATGATGATTAAGTGTGATGCTTCTCTTAAAGTGTGAAAG 1486

301 ATCAACAGCATATGATGATTAAGTGTGATGCTTCTCTTAAAGTGTGAAAG 360

1487 ACTTATGGCTTGTTCATCACTAGAGATGAGATGCGAATTTGCTAAAGCTT 1546

361 ATTGATGGCTTGTTCATCACTAGAGATGAGATGCGAATTTGCTAAAGCTT 420

1547 CATTAATCTGTCATCCCAAGAGAGATGATGCTTCTCTCAAAATCAAGGCT 1606

421 CATTAATCTGTCATCCCAAGAGAGATGATGCTTCTCTCAAAATCAAGGCT 480

1607 TAAGATTCCTGTTCTTGGGAGCTGATGATGATGCAAGTATGATGCAAT 1666

481 TAAGATTCCTGTTCTTGGGAGCTGATGATGATGCAAGTATGATGCAAT 540

1667 TGACATGATGATGCAAGTATGATGATGCAAGTATGATGCAATGATG 1726

541 TGACATGATGATGCAAGTATGATGATGCAAGTATGATGCAATGATG 600

1727 CAATCAATGAGACCTTATCAATCAATCAATCAATCAATCAATCAATCAAT 1786

601 CAATCAATGAGACCTTATCAATCAATCAATCAATCAATCAATCAATCAAT 660

1787 CATTAATGATGATGCAAGTATGATGATGCAAGTATGATGCAATGAT 1824

661 CATTAATGATGATGCAAGTATGATGATGCAAGTATGATGCAATGAT 698

RESULT 6

AU094664 689 bp mRNA linear EST 03-APR-2002

LOCUS AU094664 Rice panicle (longer than 10cm) Oryza sativa (japonica)

DEFINITION cultivar-group) cDNA clone E20409, mRNA sequence.

ACCESSION AU094664

VERSION AU094664.1 GI:8857346
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukarotca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrharioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 698)
Sasaki, T. and Yamamoto, K.

Unpublished (2000)
Rice cDNA from panicle (longer than 10cm) (2000)

CONTACT: Takuji Sasaki

National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki

305-8602, Japan
Tel: 81-298-38-7441

Fax: 81-298-38-7468

Email: tsasaki@abrr.affrc.go.jp, URL: <http://rgp.dna.affrc.go.jp/PROJECT> = "RGP"

FEATURES

source

1..689
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ORIGIN

Query Match 21.9%; Score 558.6; DB 9; Length 689;
Best Local Similarity 96.2%; Pred. No. 1.6e-133;
Matches 612; Conservative 0; Mismatches 19; Indels 5; Gaps 4;

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1 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60

1976 TTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2033

61 TTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 119

2034 GCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2093

120 GCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 179

2094 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2153

180 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 239

2154 CTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2213

240 CTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 299

2214 GTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2273

300 GTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 359

2274 TCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2333

360 TCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 419

2334 CAAGCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2393

420 CAAGCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 478

2394 GTGACACCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2453

479 GTGACACCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 538

2454 ATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2513

Db 539 ATGTAATAGTAATTCAGTTCTGAGAACTTGTGATCAACAGCGCTATGTTGTTAT 598

QY 2514 GAGCGATTAACATCTGATGATGCACTTACTAA 2549

Db 599 GAGCGATTAACATCTGATGATGCACTTACTAA 634

RESULT 7
CD869839 693 bp mRNA linear EST 11-UTL-2003

LOCUS AZ02.112M10F001124 AZ02 Triticum aestivum cDNA clone AZ02112M10,
mRNA sequence.

ACCESSION CD869839

VERSION CD869839.1 GI:32553655

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
1 (bases 1 to 693)

Genoplane.
Genoplane, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplane

COMMENT 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (<http://www.genoplane.com>
and <http://genoplane-info.infobiogen.fr>).
Location/Qualifiers
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ORIGIN

Query Match 21.9%; Score 557; DB 14; Length 693;
Best Local Similarity 87.7%; Pred. No. 4.1e-133;
Matches 608; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1284 TTAGTTCTGAGAAACATCTGCGCCATTAGTGTCTCTTATTTGTTTGAATCCGA 1343

Db 1 TTAGTTCTGAGAAACATCTGCGCCATTAGTGTCTCTTATTTGTTTGAATCCGA 60

QY 1344 CTTGATGCTTGGTTCATGATTCATCTTTGGCAATTCGAAGTGTGATGCTCTTCTTA 1403

Db 61 CTTGATGCTTGGTTCATGATTCATCTTTGGCAATTCGAAGTGTGATGCTCTTCTTA 120

QY 1404 AAGGTGAAAAGAGTATCAGATCAACAGATATGATAGTATTAATGATGCT 1463

Db 121 AAGGTGAAAAGAGTATCAGATCAACAGATATGATAGTATTAATGATGCT 180

QY 1464 ATTCTGTATGTTGGTGAAGAACTTATGCTTGTATCAACTAGAGATGATGCA 1523

Db 181 ATTCTGTATGTTGGTGAAGAACTTATGCTTGTATCAACTAGAGATGATGCA 240

QY 1524 GATTGCTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1583

Db 241 GATTGCTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

QY 1584 GTCCTCAATCAAGGCTCACTAGATTCCTGTTCTTGGGATGCTGATGATATGC 1643

Db 301 GTCCTCAATCAAGGCTCACTAGATTCCTGTTCTTGGGATGCTGATGATATGC 360

QY 1644 CAGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1703

Db 361 CATGATATATTGACAAATCAGACATGATGATGCAAAAGATATGATGATGCA 420

QY 1704 AAAATGATTTACCCAGACAGCTGCAATGCAATGAGACCTTACTAGTTCAATGATCTT 1763

Db 421 AAAATGATTTACCCAGACAGCTGCAATGCAATGAGACCTTACTAGTTCAATGATCTT 480

QY 1764 ATGAGAGTCCAGGCTTGAACGATATTTAGTACATTAATAAAGAGATTAATAT 1823

Db 481 ATGAGAGTCCAGGCTTGAACGATATTTAGTACATTAATAAAGAGATTAATAT 540

QY 1824 TATGCTGACCTATTTGGGCAAAAGCTCTGGGATTTCCAAAGCTGTTTCAATTCATCAT 1863

Db 541 TATGCTGACCTATTTGGGCAAAAGCTCTGGGATTTCCAAAGCTGTTTCAATTCATCAT 600

QY 1884 GAGTATGTTCTATGAGCTGACATGATGATGATGATGATGATGATGATGATGATGAT 1943

Db 601 GAGTATGTTCTATGAGCTGACATGATGATGATGATGATGATGATGATGATGATGAT 660

QY 1944 CATATTCATGCTTATGAGAGTCTCATACAGAT 1976

Db 661 CATATTCATGCTTATGAGAGTCTCATACAGAT 693

RESULT 8
CA498255 714 bp mRNA linear EST 14-NOV-2002

LOCUS WHE3241_A09_A17ZT wheat meiotic anther cDNA library Triticum
aestivum cDNA clone WHE3241_A09_A17, mRNA sequence.

ACCESSION CA498255

VERSION CA498255.1 GI:24989202

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
1 (bases 1 to 714)

Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R.,
Pham, V., Rausch, C.J., Sutton, T., Woo, J. and Wilson, C.
The structure and function of the expressed portion of the wheat
genomes - Meiotic anther cDNA library
Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: anderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: T7 primer.
Location/Qualifiers
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/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Plants
were grown in a glasshouse. Anther meiotic stage was
determined by removing anthers from individual primary
florets. One anther was sacrificed for microscopic
staging, and if determined to be between (and including)
meiotic stages pre-meiosis and metaphase I, the remaining
two anthers were collected and pooled for library
construction. The tissue, total RNA, and poly(A) RNA were
prepared, cDNA synthesised, and directionally ligated into
pSPORT1 by Tim Sutton in the P Langridge Lab at the

ORIGIN

Department of Plant Science, University of Adelaide, Waite Campus, Australia. Average insert size 1.5kb. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

Query Match 21.8%; Score 556.8; DB 14; Length 714;
Best Local Similarity 86.9%; Pred. No. 4.6e-133; Indels 0; Gaps 0;
Matches 612; Conservative 0; Mismatches 92;

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11 GATGTCATGATCTTGTGCTCACTCAAGAGAGATTAAGCTTGTCTCTCAATCAATCA 70
1602 TCAACTAGATTCCTGTTCTTGGGATCTGATGATATATCCCGATATATGACAAA 1661
71 TCMAAAGATTCCTGTTCTTGGGATCTGATGATATATGATGACAAA 130
1662 TCAGCTGACATGATGATGACAAAAGCTTATGTAATGATGACAAAAGCTTATCCAGCA 1721
131 TCAGCAGACATGATGATGACAAAAGCTTATGTAATGATGACAAAAGCTTATCCAGCT 190
1722 GCTTCGATGACATGATGACAAAAGCTTATGTAATGATGACAAAAGCTTATCCAGCT 1781
191 GCTTCGATGACATGATGACAAAAGCTTATGTAATGATGACAAAAGCTTATCCAGCT 250
1782 GACGACATATGATGATGACAAAAGCTTATGTAATGATGACAAAAGCTTATCCAGCT 1841
251 AATGACATATGATGATGACAAAAGCTTATGTAATGATGACAAAAGCTTATCCAGCT 310
1842 CACAAAGCTCTGGGATTTCCAAAAGCTTATGTAATGATGACAAAAGCTTATCCAGCT 1901
311 CATAAAGATTTGGGCTTACCCGAAAGCAATTCATTAATGAGTACAGTTCTATGCT 370
1902 TGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1961
371 TGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
1962 AGTGTCTATACAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2021
431 AGTGTCTATACAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
2022 AGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2081
491 CAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
2082 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2141
551 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
2142 GGTGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2201
611 GGTGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670
2202 GGTGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2245
671 GGTGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714

RESULT 9
CA754084 620 bp mRNA linear EST 27-NOV-2002
LOCUS BR040010000 PLATE_D06_44_048.ab1 OR *Oryza sativa* (japonica) cultivar-group) cDNA clone BR040010000 PLATE_D06_44_048.ab1 similar to Delta 1-pyrroline-5-carboxylate synthetase (P5CS) [includes], mRNA sequence.

ACCESSION CA754084
VERSION CA754084.1 GI:25798187
KEYWORDS EST.
SOURCE *Oryza sativa* (japonica) cultivar-group)
ORGANISM *Oryza sativa* (japonica) cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

1 (Baes 1 to 620)
Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira, H., Kawasaki, S., McCallum, A., Michalowski, C.B., Palacios, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Mark Fredrickson
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217255473
Email: bohner@life.uiuc.edu.

FEATURES

source

1..620
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/note="19 h 200mm NaCl"

ORIGIN

Query Match 21.8%; Score 555.2; DB 14; Length 620;
Best Local Similarity 99.3%; Pred. No. 1.1e-132; Indels 1; Gaps 1;
Matches 558; Conservative 0; Mismatches 3;

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1 GATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
2038 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2097
61 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
2098 AGGTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2157
121 AGGTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
2158 TAACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2217
181 TAACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
2218 TGTACACCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2277
241 TGTACACCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
2278 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2337
301 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
2338 CATCTTATGCGGCAATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2397
361 CATCTTATGCGGCAATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
2398 CACCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2457
420 CACCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
2458 AATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2517
480 AATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
2518 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2549
540 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 571

RESULT 10

CAS01661

/clone.lib="Triticum aestivum FGAS: Library 3 Gate 6"
 /note="Organ: Root; Vector: pCMV.SPORT6; Root tissue from control, cold-acclimated and salt stressed wheat cultivar Norstar. 7 mRNA populations were combined before constructing the library; 7 day non-acclimated roots, 1, 23, and 53 days cold-acclimated at 4°C, and 30 minutes, 3 hours and 6 hours treated roots with 200mM NaCl. Non-acclimated and cold-acclimated plants were grown in vermiculite while salt stressed plant were grown hydroponically. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."

ORIGIN

Query Match 21.3%; Score 543.6; DB 14; Length 821;
 Best Local Similarity 86.4%; Pred. No. 1.3e-129; Indels 1; Gaps 1;
 Matches 611; Conservative 0; Mismatches 95; Indels 1; Gaps 1;

1416 GAAGCTATCATCAACACGATTTGATAGTTATGATGCTATCTCTGTAAT 1475
 115 GAAGCAATGATCAACGCAATATTTGATAGTTATGATGCTATCTCTGTAAT 174
 1476 GTTGGTGAACAACTATTGCGCTTGTACTAGATGAGTGGAGATTGCTAAG 1535
 175 GTTGGCGAATAATTGATGGCTTATCAATAGATGAAATTCGGATTGCTAAG 234
 1536 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1594
 235 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 294
 1595 CAAGCGCTCACTAAGATTCTCTGTTGCGCATGCTGATGATATCCGATATAT 1654
 295 CAATCATCAACAAAGATTCCTGTTCTGGCCATGCTGATGATGATGATGAT 354
 1655 TGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1714
 355 TGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 414
 1715 CCACAGCGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1774
 415 CCACAGCGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 474
 1775 AGGCGCTGACGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1834
 475 AGACTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534
 1835 TATTGGCAACAAGCTGCGGATTTCCAAAGCTGTTTCAATTCATGATGATGAT 1894
 535 TGTGGCGATTAAGTATGGGCTACCAAAAGCAATTCATTCATGATGATGATGAT 594
 1895 TATGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1954
 595 TATGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654
 1955 TATGGAAGTGTCTATACAGATTTGATGATGATGATGATGATGATGATGATGAT 2014
 655 CATGGAAGTGTCTATACAGATTTGATGATGATGATGATGATGATGATGATGAT 714
 2015 TCTAGCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2074
 715 TCTAGCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774
 2075 GGGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2121
 775 TGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821

RESULT 12
 CA131282 1052 bp mRNA linear EST 24-SEP-2003
 LOCUS SCBPR1069F07.9 RT1 Saccharum officinarum cDNA clone SCBPR1069F07
 DEFINITION 5' mRNA sequence.
 ACCESSION CA131282

VERSION

CA131282.1 GI:35015111

KEYWORDS

Saccharum officinarum

SOURCE

Saccharum officinarum

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE

1 (bases 1 to 1052)
 Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
 The libraries that made SUCEST

AUTHORS

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

TITLE

Centro de Biologia Molecular e Engenharia Genetica

JOURNAL

Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089

COMMENT

Email: patricia@unicamp.br
 clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fca.v.unicamp.br
 Plate: 069 row: F column: 07
 Seq primer: T7 Promoter Primer.

FEATURES

Location/Qualifiers

source

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clone_lib

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note

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ORIGIN

Query Match 21.3%; Score 542.6; DB 13; Length 1052;
 Best Local Similarity 77.7%; Pred. No. 2.7e-129; Indels 2; Gaps 2;
 Matches 681; Conservative 0; Mismatches 194; Indels 2; Gaps 2;

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 1351 CTTGGTCAAGTTCATCTTGGCAATTCGAAGTGTATAGTCTTCTCTTAAAGGTG 1410
 75 CTTGGTCAAGTTCATCTTGGCAATTCGAAGTGTATAGTCTTCTCTTAAAGGTG 134
 1411 GAAAGAGCTATCAGATCAACACAGATTTGATGATGATGATGATGATGATGATGAT 1470
 135 GAAAGAGCTATCAGATCAACACAGATTTGATGATGATGATGATGATGATGATGAT 194
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 195 GCAACGTTGTTGAAAACTTATTTGCTTTGTTCAACTAGAGTGAATGCGAATTTGC 254
 1531 TAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1590
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 315 AAATCAAGGCTCACTAAGATTCCTGTTCTGGCATGCTGATGATGATGATGATGAT 374
 1651 ATATGACAAATGACGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710

Email: stein@ik-gatersleben.de
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ORIGIN

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 Matches 593; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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1533 AAGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1592
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361 ATTGACAAATCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 420
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421 TACCCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
1773 CCAAGCTTGAAGCATTTAGTATGATGATGATGATGATGATGATGATGATGAT 1832
481 CCAAGCTTGAAGCATTTAGTATGATGATGATGATGATGATGATGATGATGAT 540
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Db 601 TTTATGCTTGCACAGCTTGAAGTATGATGATGATGATGATGATGATGATGAT 660
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 VERSION CD919380.1 GI:32767144
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 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticaceae; Triticum.
 1 (bases 1 to 749)
 REFERENCE
 AUTHORS Genoplante.
 TITLES Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).
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FEATURES

source

ORIGIN

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 Matches 621; Conservative 0; Mismatches 98; Indels 2; Gaps 2;

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QY 2063 ATTCTCTGATGGGCGCTGTTTGGATTGGGTCTGAGTTGGCAT-AAAGCAGAGGCGTA 2121
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Job time : 5827.64 secs

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Matches 2549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	2076	GCTCGTTTGGATTTGGGTGCTGATGTTGGCATTAAGCACAGGCGCTATCCATGCCCGTGA	2135
Db	2103	GCTCGTTTGGATTTGGGTGCTGATGTTGGCATTAAGCACAGGCGCTATACATGCTGTGG	2162
Qy	2136	CCAGTGGGTGTTGAAGTCTCTTAACTACAGATGATCTTTCGAGACGTGGCAAGTG	2195
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/ Sequence 5243, Application US/10425114
/ Publication No. US20040034888A1
/
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114

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; SEQ ID NO 5243
; LENGTH: 2447
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700449031_FLI
US-10-425-114-5243

Query Match          54.7%   Score 1395.2   DB 12; Length 2447;
Best Local Similarity 76.7%   Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 518; Indels 0; Gaps 0;

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QY	634	TAGCAGACTGTTGGCACTGGAACGTGAAGCTGATCTCTTATTTGTCAGTATGTGG	693
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QY	694	ATGGTGTATATGTGTCTCACCAAGTGAACATCATCAAAAATCATACACTTATATTA	753
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QY	754	AAGAAACCATCAGCAMAAATCACTTTTGAGACAATCTCTGTAGTATAGAGAGCA	813
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QY	874	CAAGTGGGTTGAAATATGAGACATCTTAAAGTCTTCATGGGAAAAAATTGGTACTC	933
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 QY 1234 TGAAG 1293
 DB 1155 TGAAG 1214
 QY 1294 AGAAG 1353
 DB 1215 AGAAG 1274
 QY 1354 TGAATTAAG 1413
 DB 1275 TGAATTAAG 1334
 QY 1414 TGAATTAAG 1473
 DB 1335 TGAATTAAG 1394
 QY 1474 TGAATTAAG 1533
 DB 1395 TGAATTAAG 1454
 QY 1534 TGAATTAAG 1593
 DB 1455 TGAATTAAG 1514
 QY 1594 TGAATTAAG 1653
 DB 1515 TGAATTAAG 1574
 QY 1654 TGAATTAAG 1713
 DB 1575 TGAATTAAG 1634
 QY 1714 TGAATTAAG 1773
 DB 1635 TGAATTAAG 1694
 QY 1774 TGAATTAAG 1833
 DB 1695 TGAATTAAG 1754
 QY 1834 TGAATTAAG 1893
 DB 1755 TGAATTAAG 1814
 QY 1894 TGAATTAAG 1953
 DB 1815 TGAATTAAG 1874
 QY 1954 TGAATTAAG 2013
 DB 1875 TGAATTAAG 1934
 QY 2014 TGAATTAAG 2073
 DB 1935 TGAATTAAG 1994

QY 2074 GAGGCTGTTTGGATTTGGGAGTGGAGTGGCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2133
 DB 1995 GAGGCTGTTTGGATTTGGGAGTGGAGTGGCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2054
 QY 2134 GAGGCTGTTTGGATTTGGGAGTGGAGTGGCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2193
 DB 2055 GAGGCTGTTTGGATTTGGGAGTGGAGTGGCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2114
 QY 2194 GAGGCTGTTTGGATTTGGGAGTGGAGTGGCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2253
 DB 2115 GAGGCTGTTTGGATTTGGGAGTGGAGTGGCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2174
 QY 2254 GAGGCTGTTTGGATTTGGGAGTGGAGTGGCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2313
 DB 2175 GAGGCTGTTTGGATTTGGGAGTGGAGTGGCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2234
 QY 2314 CTTT 2317
 DB 2235 TATT 2238

RESULT 4

US-10-425-114-4280
 ; Sequence 4280, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhou, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kowalick, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack B.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21 (5313) B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 4280
 ; LENGTH: 2418
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700352413_FLI
 ; US-10-425-114-4280

Query Match 54.4%; Score 1386.8; DB 12; Length 2418;
 Best Local Similarity 76.8%; Pred. No. 0;
 Matches 1694; Conservative 0; Mismatches 512; Indels 0; Gaps 0;

QY 94 TCGCATGCGAGCGTGCACCCGTCGAGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 153
 DB 76 TCGCATGCGAGCGCGCGATCCGCGCGATTCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
 QY 154 TCGAGTGGGCACTGAGAGTGTCTCCAG 213
 DB 136 TCGAGTGGGCACTGAGAGTGTCTCCAG 195
 QY 214 GAGCTGTGCGAG 273
 DB 196 GAGCTGTGCGAG 255
 QY 274 CCGAGTGGTGTGAG 333
 DB 256 CCGAGTGGTGTGAG 315
 QY 334 GCTTGTGATCTGAG 393
 DB 316 GCTTGTGATCTGAG 375
 QY 394 GTCAGAGTGAATGAG 453
 DB 376 GTCAGAGTGAATGAG 435

454 CTCACTTTCTTGCACCGAGATGATTTGAGAACCCAAAGTCCGGAGCACTACTG 513
436 CTCAACTCTTGTGACCGATCGATGATTTCAAGATCCAAAGTTTGGGAGCAAGCTCCGG 495
514 AAATGTTGAGTCACTTATAGATCTTAAAGTATACCAATATTTAATGAAGATGATGCA 573
496 AGACTGTTTTCACCTTATAGATCTTAAAGTATACCAATATTTAATGAAGATGATGCA 555
574 TCAAGTATGAGAGGCTTCATATGAGATTCATGATGATTTCTGGAGTATGACAGTT 633
556 TCAATACCCGAGACAGCCATATGAGATTCATGATGATTTCTGGAGTATGACAGTT 615
634 TAGAGAGTGTGGGACCTGAGATGATGATTCCTTATTTCTGATGATGATG 693
616 TAGAGCTCTGTTGGACGAGACTTATATGATGATTTCTTATGATGATGATG 675
694 ATGGGTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 753
676 AAGAGCTCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 735
754 AAGAAAGCATGACGAGAAATATCTTTGAGAGCAATCTGATGATGATGATGATGATG 813
736 ATGAAAGCATGAGAGCAATATGATGATGATGATGATGATGATGATGATGATGATG 795
814 TGACAGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 873
796 TGACAGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 855
874 CAATGAGTGTGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATG 933
856 CAATGAGTGTGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATG 915
934 TCTTCAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 993
916 TTTTCCACAGAGCAATTTTGGGATGATGATGATGATGATGATGATGATGATGATG 975
994 CTGTTCCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1053
976 CAGTTCCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1035
1054 AGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1113
1036 AGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1095
1114 ATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1173
1096 ATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1155
1174 TGACTATTAACCGAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATG 1233
1156 TGACCTTAACCGAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATG 1215
1234 TGAGAGCCCTATTAACCGAGAAAGTATGATGATGATGATGATGATGATGATGATG 1293
1216 TGAGAGCCCTATTAACCGAGAAAGTATGATGATGATGATGATGATGATGATGATG 1275
1294 AGAAAGCATCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1353
1276 AGAAAGCATCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1335
1354 TGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1413
1336 TGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1395
1414 AAGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1473
1396 AAGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1455
1474 ATGTTGGGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1533
1456 CTGTTGGGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1515

1534 AGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1593
1516 CGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1575
1594 TCAAGGCTCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1653
1576 TCAAGGCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1635
1654 TTGACCAATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1713
1636 TTGACCAATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1695
1714 ACCAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1773
1696 ATCCAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1755
1774 CAGGCTTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1833
1756 AGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1815
1834 CTATTCGAGCAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1893
1816 CTGTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1875
1894 CTATTCGAGCAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1953
1876 CAATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1935
1954 GTTATGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2013
1936 GTTATGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1995
2014 TTCTACGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2073
1996 TTCTACGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2055
2074 GGGCTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2133
2056 GAGCCGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2115
2134 GACCAAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2193
2116 GACCAAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2175
2194 TGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2253
2176 TGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2235
2254 AAATGCTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2299
2236 AAATGCTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2281

RESULT 5
US-10-425-114-32617
Sequence 32617, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David R.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32617
LENGTH: 2563
TYPE: DNA

ORGANISM: Zee mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLM017010E08_F01
US-10-425-114-32617

Query Match 54.4%; Score 1386.8; DB 12; Length 2563;
Best Local Similarity 76.8%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 512; Indels 0; Gaps 0;

94 TCGCCATGCGAGCGTCGACCCGTCGAGCTTGTGAGGAGCGTGAAGCGCTGATCA 153
Db TCGCCATGCGAGCGTCGACCCGTCGAGCTTGTGAGGAGCGTGAAGCGCTGATCA 190
131 TCGCCATGCGAGCGTCGACCCGTCGAGCTTGTGAGGAGCGTGAAGCGCTGATCA 190
Qy TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 213
Db TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 250
191 TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 250
Qy TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 273
Db TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 310
251 GTTCTCTGTGAAACAGGTGAAGCACTGAATTTTCAAGGGTATGAGGTGATTCGTGA 310
Qy TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 333
Db TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 370
311 CCGCAGAGCTGTGGTGTGGAGGCAAGGCTCCAAATCCGTAACCTTATCCATGACA 370
Qy GCTTCTGATCTGCAAAAGCCACAGATGAGTGAAGGCTTGGGCAAGGTTG 393
Db GCTTCTGATCTGCAAAAGCCACAGATGAGTGAAGGCTTGGGCAAGGTTG 430
371 GCTTCTGATCTGCAAAAGCCACAGATGAGTGAAGGCTTGGGCAAGGTTG 430
Qy GTGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 453
Db GTGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 490
431 GTGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 490
Qy GTGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 513
Db GTGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 550
491 GTGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 550
Qy AAACTGTGATGATATTAGATCTTAAAGTTAAACAAATTTTAAAGTAAAGTGA 573
Db AAACTGTGATGATATTAGATCTTAAAGTTAAACAAATTTTAAAGTAAAGTGA 610
551 AGACTGTGATGATATTAGATCTTAAAGTTAAACAAATTTTAAAGTAAAGTGA 610
Qy TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 633
Db TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 670
611 TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 670
Qy TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 693
Db TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 730
671 TCGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 730
Qy ATGGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 753
Db ATGGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 790
731 ATGGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 790
Qy AAGAAAGCATGCAAGAAATATCTTTTGAAGACAAATCTGATGATGAGGAGCA 813
Db AAGAAAGCATGCAAGAAATATCTTTTGAAGACAAATCTGATGATGAGGAGCA 850
791 AAGAAAGCATGCAAGAAATATCTTTTGAAGACAAATCTGATGATGAGGAGCA 850
Qy TGAAGCAAAAGTGAAGGCTGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 873
Db TGAAGCAAAAGTGAAGGCTGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 910
851 TGAAGCAAAAGTGAAGGCTGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 910
Qy CAGGTGGGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 933
Db CAGGTGGGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 970
911 CAGGTGGGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 970
Qy TCTTTCACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 993
Db TCTTTCACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1030
971 TCTTTCACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1030
Qy CTTTTCACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1053
Db CTTTTCACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1090
1031 CTTTTCACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1090

Qy AGATATTGCTAGATGTTGCAAGATGCTTGGAGGCAATATGAGATTTAATAGCTGAGA 1113
Db AGATATTGCTAGATGTTGCAAGATGCTTGGAGGCAATATGAGATTTAATAGCTGAGA 1150
1091 AGATATTGCTAGATGTTGCAAGATGCTTGGAGGCAATATGAGATTTAATAGCTGAGA 1150
Qy ATGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1173
Db ATGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1210
1151 ATGAGGTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1210
Qy TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1233
Db TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1270
1211 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1270
Qy TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1293
Db TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1330
1271 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1330
Qy AGAAAGCATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1353
Db AGAAAGCATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1390
1294 AGAAAGCATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1390
Qy AGAAAGCATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1413
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1331 AGAAAGCATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1450
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1473
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1510
1414 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1510
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1533
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1570
1474 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1570
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1593
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1630
1511 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1630
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1653
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1690
1534 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1690
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1713
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1750
1571 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1750
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1773
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1810
1714 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1810
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1833
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1870
1751 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1870
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1893
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1930
1811 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1930
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1953
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1990
1834 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 1990
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2013
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2050
1894 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2050
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2073
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2110
2014 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2110
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2133
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2170
2051 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2170
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2193
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2230
2111 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2230
Qy TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2253
Db TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2290
2134 TGGTTCAGATTTGCAATCTTGGGCACTGAGGTGTCTCCAGACAGATGGAAGATGGCTTGGGCAAGGTTG 2290

1179 ATAAACCAAGAGATGACAGACCTTGCAGAAATCTATGCTACCTTGCAGAAATGGA 1238
 1081 ATGAAGCCTGGAGAAATCTCAAGCCTTGCAGCTTCCGCTCCAGCTAGCGAAATGGA 1140
 1239 GACCTATTAACAGATCTTAAAGAGACAGAGGTGTGATGATTTAGTTCTTGAGAAA 1298
 1141 GATCCAAATAGCCCGTGTATTAAGAAATCTCAGGTGAGATGATCTTATTTAGAGAG 1200
 1299 ACATCTGCCATTAAGTGTCTCTTAATTTGTTGATCCGACCTGATGCTTGGTT 1358
 1201 ACCATCAACCAATAGGTGTCTCTTAATTTGATCCGACCTGATGCTTGGTT 1260
 1359 GAGATGATCTTGGCAATTCAGAGGTGATGATGCTCTCTCAAAAAGTGAAGAAA 1418
 1261 CAGGTATCTTCCCTGCAATCCGAGTGAATGATCTTCTGCTGAGAGGTGAAGAG 1320
 1419 GCTATCAGATCAACAGATTAATGATGATTAATGATGATTAATCTCTGATGAT 1478
 1321 GCTCGATCAATAGATCTTAACAAGGTGATCACTGATGATTAATCCGAGACTGTT 1380
 1479 GGTGAAAACTTATGGCTTGTACACTAGAGATGATGATGATGATGATGATGAT 1538
 1381 GAGGTAACTCATAGACTGTGATCTCAAGAGAGAGATCTGATTTCTCAAGCTT 1440
 1539 GATGATGATGATCTTGTCTCACTCAAGAGAGAGATTAATGATGATGATGATGAT 1598
 1441 GATGATGATGATCTTGTCTCACTCAAGAGAGAGATTAATGATGATGATGATGAT 1500
 1599 GGTCACTAATGATCTGTTCTTGGGATGATGATGATGATGATGATGATGATGAT 1658
 1501 AACTGACCAAAATCCAGTGTAGCCATGCTGATGATGATGATGATGATGATGAT 1560
 1659 AATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1718
 1561 AAGTCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 1719 GAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1778
 1621 GAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 1779 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1838
 1681 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 1839 GCGCAAAAGCTCTGGATTTCCAAAGCTGTTCAATTCATGATGATGATGATGATGAT 1898
 1741 GCAAGTCAAAAGCTGATTCGGAACCAAAATCATTTCAACAGATGATGATGATGATGAT 1800
 1899 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1958
 1801 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 1959 GGAAGTCTCATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2018
 1861 GGAAGTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 2019 CGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2078
 1921 CGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 2079 CGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2138
 1981 AGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 2139 GTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2198
 2041 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 2199 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2242
 2101 GAT 2144

RESULT 8
 US-09-938-842A-1866
 ; Sequence 1866, Application US/0938842A
 ; Publication No. US20040009476A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO: 1866
 ; LENGTH: 2181
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1866
 Query Match 43.0%; Score 1096; DB 11; Length 2181;
 Best Local Similarity 69.4%; Pred. No. 2,6e-296;
 Matches 1489; Conservative 0; Mismatches 655; Indels 0; Gaps 0;
 99 ATGGCAGGCTGACCCGCTCCGAGCTTGTGAGGAGCTGAAGCGCTCATCATCAAG 158
 1 ATACCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 159 GTGGGACATGAGCTGCTCCAGACAGATGATGATGATGATGATGATGATGATGATGAT 218
 61 GTTGGACATGAGCTGCTCCAGACAGATGATGATGATGATGATGATGATGATGATGAT 120
 219 CTGTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278
 121 ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 279 GGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 338
 181 GGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 339 GGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 398
 241 GCAGATTTACAGAGCCCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 399 AGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 458
 301 AGCAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 459 CTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 518
 361 ATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 519 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578
 421 GTCAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 579 ACTGAAGGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
 481 ACTGCAAGGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 639 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
 541 GCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 699 TTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 758

Db 601 CTTTACCTGGCCCTCCAGTGAATTTACTCTCAAAATTAATACCAATTCATTAAAGAA 660
 Qy 759 AAGCATGCAAGAAATCACTTTTGAGACAAATTCGTGTAGGTAGAGAGCATGACA 818
 Db 661 AAACCCAGAGAGATTAATTTGGCGAAAGTCCAAATTAAGAGAGAGGATGACT 720
 Qy 819 GCAAAAGTGAAGGCTGTCTGTCTTCAATAGCGGACACCTGTGTATTAACAGT 878
 Db 721 GCAAAAGTGAAGGCTGTCTGTCTTCAATAGCGGACACCTGTGTATTAACAGT 780
 Qy 879 GGGTTTGAAGAAATCGAGCATTTAAAGTCTTCATGCGGAAAAAAATTTGACTCTTT 938
 Db 781 GGAATGAGAGTGAATTAAGTAAAGTCTTGAAGAGACGCGTGTGGTGAACCTGTTTC 840
 Qy 939 CACAAAGTGGCAATTTGTGGGAATCATCTAAGATGTAGTACTCTGTAGATGGCTGTT 998
 Db 841 CATCAAGATGCTCATTTATGGGCTCCGGTCTGATGATCTCTTCTGTGACATGGCAGTT 900
 Qy 999 GCCCGAAGAGATTTGTCAAGGATCTACAGAAATTTGTCTACAGAGAGAGAAAAAGATA 1058
 Db 901 GCTGTAAGAGAAAGTCAAGAAAGTTCAGGCTTATCTTGAAGAGATAGAAACAATTT 960
 Qy 1059 TTGCTAGATGTTGAGATGCTTTTGAGGCAATGAGATTAATPAAGGTGAGATGAA 1118
 Db 961 CTACACGACATTTGCCAATGCCCTTGAAGTAAATGAGAAACAAATTAAGCTGAGAAATGAT 1020
 Qy 1119 GCTGATGATGCTGGCGCCCAAGTTGCTGATATGAGAGCTTTGGTTGCTGATGATGACT 1178
 Db 1021 TTGATGTTGCTGACGACCAAGAAAGTGAATGAGAGTCTTGGTGTGCTGCTTGGT 1080
 Qy 1179 ATAAACCAAGAAAGATGACAAAGCTTGAATCTTCTGACCTTGAATATGAA 1238
 Db 1081 ATGAAGCCTGGGAAATCTCAAGCTTTCAGCTTCGTTGCCAGCTGAGCGAAATGAA 1140
 Qy 1239 GACCTATTAACAGATCTTAAAGACAGAGTGTCTGATGATTAAGTCTTGAAGAA 1298
 Db 1141 GATCCAAATAGGCGGTGTAAAGAACTCAGGTGAGATGATCTTATTTTGAAGAG 1200
 Qy 1299 ACATCTTGCCCATGAGTGTCTCTTAAATGTTTGAAGTCCCACTGATGCTTGGT 1358
 Db 1201 ACCTATCAACCAATGAGTGTCTTGAATGTTTGAATGCCGCTGATGACCTTGGT 1260
 Qy 1359 CAGATGCACTTTTGCAATTCAGAGGTGAATGCTTCTCTTAAAGGTGAGAAAGAA 1418
 Db 1261 CAGGATATCTTCTGCAATCGAGGTGAATGCTTCTCTGCAAGGAGTGAAGAG 1320
 Qy 1419 GCTATCAAGTCAACAGATTTGATAGAGTGAATGATGATGATGATGATGATGAT 1478
 Db 1321 GCTGCTGATCAAAAGTCTTATCAACAGGATGATGATGATGATGATGATGATGAT 1380
 Qy 1479 GGTGAAAAATTTGGCTTGTTCACATGAGATGATGATGATGATGATGATGATGAT 1538
 Db 1381 GGAGGTAATCTATGAGACTTGTGACCTCAAGAGAGAGATGATGATGATGATGATGAT 1440
 Qy 1539 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1598
 Db 1441 GATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Qy 1599 GGTCACTAAGATTCCTGTTCTTGGGCACTGATGATGATGATGATGATGATGATGATGAT 1658
 Db 1501 AACTGAGAGAAATCCAGTGTAGGCACTGATGATGATGATGATGATGATGATGATGAT 1560
 Qy 1659 AATTCAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1718
 Db 1561 AAGTCTGATTAAGTGAATGAGCAAGCATGATGATGATGATGATGATGATGATGATGAT 1620
 Qy 1719 GAGGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1778
 Db 1621 GAGGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Qy 1779 CTTGACGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1838

Db 1681 CTCGATGATCTTATTTATGTTCTGCAACCAAGGCGTCACTTTGTATGTGGCCAGA 1740
 Qy 1839 GCGCAACAAAGCTGTGGATTTCCAAAGCTGTTTATTTATCATGATGATGATGATGATGATGAT 1898
 Db 1741 GCAAGTGCACAACTAATATTCGGAACCAAAATCATTTTCACAGAGATGATGATGATGATGATGAT 1800
 Qy 1899 GCTGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1958
 Db 1801 GCTGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 Qy 1959 GGAAGTCTCATCAAGATTTGATGCTCACTACAGATGATGATGATGATGATGATGATGATGAT 2018
 Db 1861 GGAAGTCTCATCAAGATTTGATGCTCACTACAGATGATGATGATGATGATGATGATGATGAT 1920
 Qy 2019 CGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2078
 Db 1921 CGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Qy 2079 CGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2138
 Db 1981 AGGTTGCACTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 Qy 2139 GTGGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2198
 Db 2041 GTGGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 Qy 2199 AATGTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2242
 Db 2101 GATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2144

RESULT 9
 US-09-938-842A-1391
 : Sequence 1391, Application US/09938842A
 : Patent No. US20020160378A1
 : GENERAL INFORMATION:
 : APPLICANT: Harper, Jeff
 : APPLICANT: Krepes, Joel
 : APPLICANT: Wang, Xun
 : APPLICANT: Zhu, Tong
 : TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 : TITLE OF INVENTION: SAME, AND METHODS OF USE
 : FILER REFERENCE: S091300-3
 : CURRENT APPLICATION NUMBER: US/09/938, 842A
 : CURRENT FILING DATE: 2001-08-24
 : PRIOR APPLICATION NUMBER: US 60/227, 866
 : PRIOR FILING DATE: 2000-08-24
 : PRIOR APPLICATION NUMBER: US 60/264, 647
 : PRIOR FILING DATE: 2001-01-16
 : PRIOR APPLICATION NUMBER: US 60/300, 111
 : PRIOR FILING DATE: 2001-06-22
 : NUMBER OF SEQ ID NOS: 5379
 : SEQ ID NO 1391
 : LENGTH: 2154
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 : US-09-938-842A-1391

Query Match 42.6%; Score 1085.6; DB 9; Length 2154;
 Best Local Similarity 69.1%; Pred. No. 2,1e-293;
 Matches 1484; Conservative 0; Mismatches 664; Indels 0; Gaps 0;

Qy 99 ATGGCGAGGCTGACCGTCCCGAGCTTCGTAAGGAGAGTGAAGCGCTCATCATCAAG 158
 Db 1 ATGGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 Qy 159 GTGGGCACTGAGTGTCTCCACAGAAATGAGAAATTTGCTTTGGGCAAGGTTGAGCT 218
 Db 61 GTTGGGCAAGCAAGTGTCTTCTGAAAAGGTGAAGATTGGCTCTTGTGTGATGAGCA 120
 Qy 219 CTGTGGAGAGGTTTAAAGAACTGATCTTTTGAATGAAGATGATGATGATGATGATGATGATGAT 278
 Db 121 CTGTGTGACAGCTTGGGAAATTAATCGATGATGATGATGATGATGATGATGATGATGATGAT 180

279 GGTGCTGTGAGTGGGGGCGACGACCTAGTACCGGAAAGCTTGTCAATAGACGCTT 338
Db 181 GGTGGCGTGTGCTTGGCGAGGCAAGGCTTGTATGACATATAGTCAATAGACGCTT 240
Qy 339 GGTGATTCGCAAAAGCCAGATGAGTGTAGTGAAGGCTTGGCGGCTTGGTGTAG 398
Db 241 GCGGATCTTCAAGAGCTCAGACTGAACTTGATGGAAAGGCTTGGTGTGTGACAA 300
Qy 399 AGTGAAGTATGAGCTCTTACGATATGTTGTTAAACCACTGATGTCTGTCACTTCA 458
Db 301 AGGAGCTTATGCTTACTACTATAGACTATGTTGACGAGCTTATGATGACGCGACCTCA 360
Qy 459 CTCTTGTCAACGACGATATTTGAGAACCAAGTTCCGGAGCACTCACTGAACT 518
Db 361 CTCTGAGTAAATGACAGTATTTTGAAGCAAGATTTCAAGAACCACTTAAATGAACT 420
Qy 519 GTTGAATCATTTATGATCTTAAAGTTATACCAATTTTAAATGAATGATGCCATCAG 578
Db 421 GTCAAGCTATGCTTATGATTTGAGGGTATTCATTTTCAATGAGAAATGATGCTATAGC 480
Qy 579 ACTGAAAGGCTTCATATGAGATTCATGTTATTTCTGGGATATGACAGTTTACCA 638
Db 481 ACCCGAAGGCCCATATCAGATCTTCTGATTTCTGGGATATGAGATGAGTACTAGCT 540
Qy 639 GAGCTGTGGCACTGGAAGCTGATCTCTTATCTGCTCAGATGATGATGAGG 698
Db 541 GCTCTTCTGCGCTTGAAGCTGAAAGCTGATCTTCTGATTTCTTGAAGGATGTTAAAGT 600
Qy 699 TTGTATAGTGTGCAACCAAGTGAACCATCATCAAAATCAACACATTTATTAAGAA 758
Db 601 CTTTACACAGGCGCTTCAAGTATCTTAACTCAAGTTGATCCACATTTGTTAAAGAA 660
Qy 759 AAGCATCAGCAAGATTCATTTTGAAGCAATCTGCTGATGATGAGAGGAGCA 818
Db 661 AAACATCAGATATGATTCATTTGCGGACCAATCAAGTTGAGGAGAGGAGTATGACT 720
Qy 819 GCAAAAGTGAAGGCTGCTGCTTGGCTTCAATAGGCGACACTGTGTTATTAACAAGT 878
Db 721 GCAAAAGTGAAGGCTGCTGCTTGGCTTCAATAGGCGACACTGTGTTATTAACAAGT 780
Qy 879 GGGTGTGAAGATGAGGATTTCTTAAGTCTTCAATGAGGAGGAGGAGGAGTCTCTT 938
Db 781 GGGTATTCAGCTGAGACATATGATTAAGTCTTCAAGGAGCTGCTGTTGAAGCTTGT 840
Qy 939 CACAAAGATGCGAATTTGTGAGATCATCTAAGATGATGATCTGATGATGCTGTT 998
Db 841 CATCAAGATGCTGTTATGAGGCTCCGATCAGATTCATGATGCTGATGATGCAAGT 900
Qy 999 GCGGCAAGATGTTTCAAGGATCTTCAAGATTTTCTCATGAGGAGGAGGAGGAGT 1058
Db 901 GCTGCGAGGAGGATTCAGAAAGCTTCAAGGCTTCTTGGAGAACAGGAGGAGGAGT 960
Qy 1059 TTGCTGATGTTGCAAGTCTTGAAGGCAATGAGATTTTAAATGATGATGATGATG 1118
Db 961 CTGCTGATATTTGCGATGCTTGAAGGAGGAGGATTTCAATGAGGAGGAGGAGT 1020
Qy 1119 GCTGATGATGCTGCGGCGCAAGTGTGATGATGAGAGGCTTGTGCTGATGATGAT 1178
Db 1021 TTGATGATGATGCTTGTGCAAGGAGGCTGAGTGTGAGAGGATGATGATGATGAT 1080
Qy 1179 ATAAAGCAGAGAGATGAGAGGCTTGAAGGCAATGATGATGATGATGATGATG 1238
Db 1081 ATGACACTGAGAGAGATGATGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAG 1140
Qy 1239 GAGCCTATTAACAGATTAATTAAGAGAGAGGCTGATGATGATGATGATGATG 1298
Db 1141 GATCAATGAGGCGCTGTTTAAAGAGAGAGAGGATGATGATGATGATGATG 1200
Qy 1299 AATGCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1358
Db 1201 ACCCATACACATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1260

Qy 1359 CAGATTCATCTTTGGCAATTCGAAGTGTATGATGCTTCTCTTAAAGTGAAGAG 1418
Db 1261 CAGATTCATCTTTGGCAATTCGAAGTGTATGATGCTTCTCTTAAAGTGAAGAG 1320
Qy 1419 GCTATCAGATCAACAGATTAATTCATTAAGTGTATGATGCTTCTCTTAAAGT 1478
Db 1321 GCGCGGAGATCAAGATGCTTCTTCAAGAGGATGATGATGATGATGATGATGATG 1380
Qy 1479 GGTGAAGAACTTATGAGCTTGTATCACTAAGATGATGATGATGATGATGATG 1538
Db 1381 GGGGCTTAACTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
Qy 1539 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1598
Db 1441 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Qy 1599 GCGTCAACTAAGATTCCTGTTTGGGCAATGCTGATGATGATGATGATGATG 1658
Db 1501 AATATCAAAATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1560
Qy 1659 AATATCAAAATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1718
Db 1561 AAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 1719 GAGCTGCAATGCAATGAGACCTTACTAGTATGATGATGATGATGATGATGATG 1778
Db 1621 GAGCTGCAATGCAATGAGACCTTACTAGTATGATGATGATGATGATGATGATG 1680
Qy 1779 CTGATGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1838
Db 1681 CTGATGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Qy 1839 GCGCAAAAGCTTGGGATTTCCAAAGCTGTTTCAATTCATGATGATGATGATG 1898
Db 1741 GCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Qy 1899 GCGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1958
Db 1801 GCTTGAAGCTTATTTTGTGCTGAGAGCAATGATGATGATGATGATGATGATG 1860
Qy 1959 GGAAGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2018
Db 1861 GGAAGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
Qy 2019 GCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2078
Db 1921 GCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Qy 2079 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2138
Db 1981 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
Qy 2139 GTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2198
Db 2041 GTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Qy 2199 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2246
Db 2101 GAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2148

RESULT 10
US-09-938-842A-1391
; Sequence 1391, Application US/09938842A
; Publication No US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3

CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO: 1391
LENGTH: 2154
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1391

Query Match 42.6%; Score 1085.6; DB 11; Length 2154;
Best Local Similarity 69.1%; Pred. No. 2,1e-293;
Matches 1484; Conservative 0; Mismatches 664; Indels 0; Gaps 0;

99 ATGGGAGGCTGACCCCTCCCGAGCTTCGTGAGGAGCGGTGACATCATCAAG 158
1 ATGGGAGGCTGACCTTCACGCTTTTCCAGAGCTCAACCTATGCTTAAAG 60
159 GTGGGAGGCTGACCTTCACGAGCAAGATGAGATGCTTGGGAGGCTTGAAG 218
61 GTGGGAGGCTGACCTTCACGAGCAAGATGAGATGCTTGGGAGGCTTGAAG 120
219 CTGTCGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 278
121 CTGTCGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 180
279 GATGCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 338
181 GATGCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 240
339 GCTGATCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAG 398
241 GCGGATCTTGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAG 300
399 AGTGAAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAG 458
301 AGGATCTTGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 360
459 CTTCCTTGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 518
361 CTTCCTTGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 420
519 GTTGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 578
421 GTTGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 480
579 ACTGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 638
481 ACCGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 540
639 GATGCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 698
541 GCTGCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 600
699 TTGTAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 758
601 CTTCGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 660
759 AAGCATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 818
661 AAGCATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 720
819 GGAAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 878
721 GGAAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 780
879 GGGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 938

840 781 GGGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 840
998 939 CAGGAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 998
900 841 CAGGAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 900
1058 999 GCGGAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1058
960 901 GCGGAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 960
1118 1059 TTGTAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1118
1020 961 CTTCGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1020
1178 1119 GCTGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1178
1080 1021 TTGTAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1080
1238 1179 ATGAAAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1238
1140 1081 ATGAAAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1140
1298 1239 GAGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1298
1200 1141 GATGCAAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1200
1358 1299 ACATCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1358
1260 1201 ACATCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1260
1418 1359 CAGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1418
1320 1261 CAGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1320
1478 1419 GCTATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1478
1380 1321 GCGGAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1380
1440 1381 GGGGAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1440
1598 1539 GATGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1598
1500 1441 GATGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1500
1658 1599 GCGTCAAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1658
1560 1501 AATGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1560
1718 1659 AATGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1718
1620 1561 AAGGATGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1620
1778 1719 GAGGCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1778
1680 1621 GAGGCTGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1680
1838 1779 CTTCGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1838
1740 1681 CTTCGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1740
1898 1839 GCGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1898
1800 1741 GCAAGGAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1800
1958 1899 GCGTGAAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1958
1860 1801 GCTTGAAGGAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGAT 1860
2018 1959 GGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2018
1920 1861 GGAAGGCTTGAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1920

QY 2019 CGCAGATTGATAGTCTGCTGATTTTCAATGACAGATGATCTCTGATGAGGCT 2078
 Db 1921 CGCAGATTGATAGTCTGCTGATTTTCAATGACAGATGATCTCTGATGAGGCT 1980
 QY 2079 CGTTTGGATGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2138
 Db 1981 CGATTGGATGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 QY 2139 GTGGTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2198
 Db 2041 GTGGTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 QY 2199 AATGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2246
 Db 2101 GACGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2148

RESULT 11

US-10-026-767-2
 Sequence 2, Application US/10026767
 Publication No. US20030014774A1
 GENERAL INFORMATION:
 APPLICANT: Hitachi, LTD.
 APPLICANT: RIKEN
 APPLICANT: Japan International Research Center for Agricultural Science
 APPLICANT: Bio-oriented Technology Research Advancement Institute (BRAI)
 TITLE OF INVENTION: Transgenic rice plant and its family with environmental stress resistant by proline accumulation of high level and its production.
 FILE REFERENCE: NT01P0353
 CURRENT APPLICATION NUMBER: US/10/026,767
 CURRENT FILING DATE: 2001-12-27
 NUMBER OF SEQ ID NOS: 3
 SEQ ID NO 2
 LENGTH: 2571
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 107..2260
 AUTHORS: Yoshin Yoshida, Tomohiro Kiyasue, Takeshi Karagiri, Hiroko
 AUTHORS: Ueda, Tsuyoshi Hozoguchi, Kazuo Yamaguchi-Shinozaki, Keishiro
 AUTHORS: Wada, Yoshinori Harada, Kazuo Shinozaki
 TITLE: Correlation between the induction of a gene for 1-
 TITLE: Pyroline-5-carboxylate synthetase and the accumulation of
 TITLE: proline in Arabidopsis thaliana under osmotic stress.
 JOURNAL: The Plant Journal
 VOLUME: 7
 ISSUE: 7
 PAGES: 751-760
 DATE: 1995-01-20
 DATABASE ACCESSION NUMBER: D32138
 DATABASE ENTRY DATE: 1994-07-12
 US-10-026-767-2

Query Match 42.6%; Score 1085.6; DB 14; Length 2571;
 Best Local Similarity 69.1%; Pred. No. 2,4e-293;
 Matches 1484; Conservative 0; Mismatches 664; Indels 0; Gaps 0;

QY 99 ATGCGAGCGTCCGCGCCGCGGAGCTGTCGAGGAGCTGAAGCGCTCATCATCAAG 158
 Db 107 ATGAGAGAGCTAGATCGTTCACGCTTTGCGAGAGAGCTCAAGATGATCGTTAAG 166
 QY 159 GTGGGACATGAGTGTCTCTGACACAGACAGATGAGATGAGTGTGGGAGGCTTGAAGT 218
 Db 167 GTTGGACAGAGTGTCTCTGACACAGAGATGAGATGAGTGTGGGAGGCTTGAAGT 226
 QY 219 CTGTGCGAGCAGTTAAGAACTGATCTTTAGAGATACAGATGATGATGATGATGATGAT 278
 Db 227 CTGTGCGAGCAGTTAAGAACTGATCTTTAGAGATACAGATGATGATGATGATGATGAT 286
 QY 279 GGTGCTGTGAGTGGGCGACAGCAGCTTATGATCCGGAAGCTTGTCAATATACAGCTTT 338

Db 287 GGTGCGTGTGCTCTGCGAGGCAAGGCTTCGTTATGACATTAATGATGATGATGATGAT 346
 QY 339 GCTGATCTGCAAAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 398
 Db 347 GCGGATCTTCAAGAGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 406
 QY 399 AGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 458
 Db 407 AGAGTGTATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 466
 QY 459 CTCTTGTCCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 518
 Db 467 CTCTTGTCCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 526
 QY 519 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578
 Db 527 GTCAAGTGTATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 586
 QY 579 ACTGAAGAGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
 Db 587 ACCGAGAGAGCCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 646
 QY 639 GCACTGTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 698
 Db 647 GCTCTACTGCGGTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 706
 QY 699 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 758
 Db 707 CTCTTACAGAGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 766
 QY 759 AAGCATGCAAGAAATCACTTTTGAAGCAAAATCTGATGATGATGATGATGATGATGAT 818
 Db 767 AACATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 826
 QY 819 GCAAAATGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
 Db 827 GCAAAATGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 886
 QY 879 GGGTTTGAATCGAGATCTTAAAGTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 938
 Db 887 GGGTTTGAATCGAGATCTTAAAGTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 946
 QY 939 CACAGAAATGGAATTTTGGGAAATCAATGAAGATGATGATGATGATGATGATGATGATGAT 998
 Db 947 CATGAAGTGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
 QY 999 GCCCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1058
 Db 1007 GCTGCGAGGAGAAATTCAGAAAGCTTCAGAGCTTATCTTGGAGAGCAGAGAGGAGGAG 1066
 QY 1059 TTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
 Db 1067 CTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1126
 QY 1119 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1178
 Db 1127 TTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1186
 QY 1179 ATTAACCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1238
 Db 1187 ATGAACCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1246
 QY 1239 GACCTATTAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1298
 Db 1247 GATCAATCGGCGGCTTTTAAAGAAACAGAGTGGAGATGATGATGATGATGATGATGAT 1306
 QY 1299 ACATTTGCGCATTAAGTGTCTCTTATGATGATGATGATGATGATGATGATGATGATGAT 1358
 Db 1307 ACCTCATACCAATTAAGGAGTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 1366
 QY 1359 CAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1418

Db 1367 CAGATGCTTCACTTCCGATCCGATGAGAAATGCTTTCTGCTGAAGGCTGGAAGAG 1426
 Qy 1419 GCTATCAGATCAACAACAGATATTCATATAGATTATTAATGATCTATTCCTGTAATGTT 1478
 Db 1427 GCCCGGAGATCAATGCTATCTTACACAGAGTATGATCTGATCAATTCAGAGACTGTT 1486
 Qy 1479 GGTGAAAACCTATTTGGCCTTTGTTACAACTAGAGATGAGATGCCAGATTTGCTAAAGCTT 1538
 Db 1487 GGGGGTAACTCATTTGACTTGTGACTTCAAGAAAGATTCCTGATTTGCTTAAAGCTT 1546
 Qy 1539 GATGATGCTATGATCTTGTCTCACTCCAAAGAGAGATTAATAGCTTCTCTCAATCAAG 1598
 Db 1547 GATGACGTATGATCTTGTGATCTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1606
 Qy 1599 GCGTCAACTTAAGATTCCTGTTCTTTGGGAGATGCTGATGCTATTAAGCCAGTATTAATGAC 1658
 Db 1607 AATACCTCAAAAATCCCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAC 1666
 Qy 1659 AATACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1718
 Db 1667 AAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726
 Qy 1719 GCAGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1778
 Db 1727 GCAGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
 Qy 1779 CTTGACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1838
 Db 1787 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
 Qy 1839 GCGCACAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1898
 Db 1847 GCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1906
 Qy 1889 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1958
 Db 1907 GCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1966
 Qy 1959 GGAAGTCTCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2018
 Db 1967 GGAAGTCTCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2026
 Qy 2019 CGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2078
 Db 2027 CGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2086
 Qy 2079 CGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2138
 Db 2087 CGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2146
 Qy 2139 GTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2198
 Db 2147 GTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2206
 Qy 2199 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2246
 Db 2207 GACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2254

RESULT 12
 US-10-260-238-466

/ Sequence 466, Application US/10260238
 / Publication No. US20040016025A1
 / GENERAL INFORMATION:
 / APPLICANT: Budworth, Paul R.
 / APPLICANT: Moughamer, Todd G.
 / APPLICANT: Briggs, Steven P.
 / APPLICANT: Cooper, Bret
 / APPLICANT: Glazebrook, Jane
 / APPLICANT: Goff, Stephen A.
 / APPLICANT: Katagiri, Fumiyaki
 / APPLICANT: Krepis, Joel
 / APPLICANT: Provart, Nicholas

/ APPLICANT: Rieke, Darrell
 / APPLICANT: Zhu, Tong
 / TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 / FILE REFERENCE: 60111-NP
 / CURRENT APPLICATION NUMBER: US/10/260,238
 / CURRENT FILING DATE: 2002-09-26
 / PRIOR APPLICATION NUMBER: US 60/325,448
 / PRIOR FILING DATE: 2001-09-26
 / PRIOR APPLICATION NUMBER: US 60/325,277
 / PRIOR FILING DATE: 2001-09-26
 / PRIOR APPLICATION NUMBER: US 60/370,620
 / PRIOR FILING DATE: 2002-04-04
 / NUMBER OF SEQ ID NOS: 6077
 / SEQ ID NO 466
 / LENGTH: 2214
 / TYPE: DNA
 / ORGANISM: *Oryza sativa*
 / US-10-260-238-466

Query Match 42.4%; Score 1079.6; DB 15; Length 2214;
 Best Local Similarity 73.5%; Pred. No. 1.1e-29;
 Matches 1627; Conservative 0; Mismatches 474; Indels 113; Gaps 15;

Qy 96 GCATGCGAGCGTGCACCCCTCCCGAGCTTCTGAGGAGCGTGAAGCGGCTCATATC 155
 Db 55 GACGTGAGAGACACCGACTCCACCCGCGCTTCGTCAAGAGCGTGAAGCGATCATATC 114
 Qy 156 A-----AGTGGGACCTGACATGCTCCAGACAGATGGAAGATGGCTTTG 203
 Db 115 AAGTTAATTCACAGAGTGGGACCGCTTTGTGACTGGGCGGATGGCGGTTGGCTATG 174
 Qy 204 GCGAGGATGAGCTCTGTGCGAGCGATTAAAGAACTGAATCTTTAGATACGAAGTG 263
 Db 175 GCGAGGCTGGGCTGCTGTGTGAACAG-----CTAAATTTGAGGGGTACGAGGTG 225
 Qy 264 ATTTTGTGACCTGAGGTGCTTTGAGATGGGGGCAACGCACTTAGGTAACGGAAGCT 323
 Db 226 ATTTGCTGACCTGTGAGGTGCTTTGAGATGGGGGCAAGGCTCAAGTCCGGAAGCTC 285
 Qy 324 GTCAATAGC-----AGCTTGTGATCTGCAAAAGCCACAGATGAGATTAGA 370
 Db 286 GTCAATAGAGGTTGACAGAGAGTTTGTGATCTGATCTGCAAGACCAAGATGACATGGA 345
 Qy 371 TGGAAAGCTTGTGCGCTGTTGTGATGAGATGATGATGATGATGATGATGATGATGAT 430
 Db 346 CGGGAAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 405
 Qy 431 TA---ACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
 Db 406 TACCAAGAGCTTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465
 Qy 488 CCGAAGTTCGGGAGCACTCACTGAACCTGTTGATGATGATGATGATGATGATGATGATGAT 547
 Db 466 TCCAGTTTGGGAACCGAGCTCCGAGACTGTTAATCTCTGTTAGATCCCAAGATTAT 525
 Qy 548 ACCAATATTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 607
 Db 526 ACCAATATTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
 Qy 608 TGGTATATTCTGGGATTAATGACAGTTTAGCAGACTGTTGCACTGGAATGGAAGCTGA 667
 Db 586 TGGCATATTCTGGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
 Qy 668 TTTCTTATTTGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
 Db 646 TTTCTTATTTGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 705
 Qy 728 ATCAAAATCATACACATTAATTAAGAAAGATCAAGAAATCATCTTTTGGAGA 787
 Db 706 ATGAAGATTAATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
 Qy 788 CAATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847

Db 766 GAAATCTCTGTGGAGAGGTGATGAGCTAAAGTACGCTTTTACTGCTTC 825
 Qy 848 AATATCGGCACACCTGTGGTTATAC--AGTGGGTTTGAATAATCGAGCATCTTAA 905
 Db 826 ATCAAAAGAAATACCTGTGTATGTCAGAGTGTGATGATGATGATATTAAG 885
 Qy 906 GTTCTTCATGGGAAAAAATGGTACTCTCTTCAAGAAATGCAATTTGGGAAACA 965
 Db 886 GTCATCGAGAGAGAAAAATCGTACGCTTTTCCATGAGGAAACCAAGTGGGTTGT 945
 Qy 966 TCTAAGATGTTAGTACTGATGAGATGCTGTGCGCAAGATTTGTTCAGGATCTA 1025
 Db 946 TCCAAAGGAGCAACAGCGGTGAGATGCGCTTGTGCAAGAGATTTGCTCCAGATCTA 1005
 Qy 1026 ---CAGAAATTTGTCATCAGAGAACAAAAAATTTGCTGATGATTTGGCAATCTTGG 1082
 Db 1006 CAGCAAAATTTGCTGCTAGAGAGCGTAAAGAAATTTGCTAGACATGCGCATCTCTTA 1065
 Qy 1083 GAGCAAAATGAGATTTAATTAAGGTCTGAGATGAGATGATGATGATGATGATGATGAT 1142
 Db 1066 GAGCAAAATGAGATTTAATTAAGGTCTGAGATGAGATGATGATGATGATGATGATGAT 1125
 Qy 1143 GCTGATATGAGAGGCTTTGCTGCTAGATGATGATGATGATGATGATGATGATGATGAT 1202
 Db 1126 ATGCTTACGATTAATCATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1183
 Qy 1203 CTGCAAAATCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
 Db 1184 CTGCAAGATCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
 Qy 1263 AAGACAGAGGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1322
 Db 1244 AGAACAAG-----CAATGGGTTGCTC 1267
 Qy 1323 TTAATGTTTGAAGTCCGACCTGATGCTT-----GTTCAAGTTGCTGCTGCTGCTGCTGCTGCT 1376
 Db 1268 CTATATATTTTGAAGTCCGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1327
 Qy 1377 ATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1436
 Db 1328 ATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1387
 Qy 1437 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1488
 Db 1388 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1447
 Qy 1489 TTAATGCTTGTATCACTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1548
 Db 1448 TTAATGCTTGTATCACTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1507
 Qy 1549 TTAATGCTTGTATCACTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1608
 Db 1508 TTAATGCTTGTATCACTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1567
 Qy 1609 AGATTCCTGTTCTGAGGATGCT--GATGATATGCAAGTATATGATGATGATGATGATGATGATGATGAT 1667
 Db 1568 AGATTCCTGTTCTGAGGATGCT--GATGATATGCAAGTATATGATGATGATGATGATGATGATGATGAT 1627
 Qy 1668 GACATGATATGCAAAATCTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1727
 Db 1628 GACATGATATGCAAAATCTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1687
 Qy 1728 AATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1787
 Db 1688 AATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1747
 Qy 1788 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
 Db 1748 TTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1807
 Qy 1847 AGCTCTGAT 1906
 Db 1808 CACTTGAATCACTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1867

Qy 1907 TGTGATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1961
 Db 1868 CTTGAT 1927
 Qy 1962 ---AGTCTCATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2018
 Db 1928 TTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1987
 Qy 2019 CGCAGAT 2076
 Db 1988 CAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2047
 Qy 2077 CTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2136
 Db 2048 CTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2107
 Qy 2137 CAGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2196
 Db 2108 CTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Qy 2197 TGAATGAT 2250
 Db 2161 TGAATGAT 2214

RESULT 13
 US-10-424-599-44242
 ; Sequence 44242, Application US/10424599
 ; Publication NO. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 44242
 ; LENGTH: 2499
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_13949C.1
 US-10-424-599-44242

Query Match 42.2%; Score 1076.8; DB 12; Length 2499;
 Best Local Similarity 69.7%; Pred. No. 7.1e-291;
 Matches 1509; Conservative 0; Mismatches 612; Indels 45; Gaps 2;
 Qy 99 ATGCGAGCGTGAACCCGTCGAGCTTGTGAGGAGCTGAAGCGGTCATCATCAG 158
 Db 59 ATGAGAAACAGATCTCTGAGACATTTCTCAAGATTTAAGCGCATCATATCAAG 118
 Qy 159 GTGGCACTGAGATGCTCTCCAGACAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 218
 Db 119 GTGGCACTGAGATGCTCTCCAGACAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 178
 Qy 219 CTGTCGAGCAGGTTAAGAACTGAACCTTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278
 Db 179 CTGTCGAGCAGGTTAAGAACTGAACCTTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
 Qy 279 GGTGCTGTGAGAGTGGGCGACAGCGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 338
 Db 229 GGTGCTGTGAGAGTGGGCGACAGCGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 298
 Qy 339 GCTGATCTGCAAAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 398
 Db 239 GCTGATCTGCAAAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 358

QY 399 AGTGAAGTATGCTCTTTACATATGTTGTTAAACCACTGATGTCTGCTATCTCA 458
 DB 359 AACACCTTATGCTCTTTATGATGTTGTTTACTGAGTGAATGACATCTGCTCAG 418
 QY 459 CTTCTTGTCACCGACGATGTTTGAAGAACCAAGTCCGAGAGCACTCACTGAAGT 518
 DB 419 CTTCTTGTCACCGACGATGTTTGAAGAACCAAGTCCGAGAGCACTCACTGAAGT 478
 QY 519 GTTGAATCATTTATGATCTTAAAGTATACCAATATTTAATGAATGATCCATCAGC 578
 DB 479 ATGAATCATTTGTTGACATTTAAAGTATATCCCATATTTCAACGAGAACGATGAGT 538
 QY 579 ACTGAAGAGCTCCATATGAGATTCATCTGATATTTCTGAGATTAAGACAGTTTGA 638
 DB 539 ACTGAAGAGCTCCATATGAGATTTCTTGGCATATTTTGGATTAATGACAGTTTGA 598
 QY 639 GGAATGTTGACCTGGAACCTGAAGCTGATCTCTTATTTCTGATGATGATGAGG 698
 DB 599 GCTTATTTGGCATTTGGAATTTAAAGCTGATCTTATTTGTTGATGATGATGAGG 658
 QY 699 TTGTATAGTGTCCACCAAGTGAACCATCAACAAATATCACTATATTAAGAA 758
 DB 659 CTTATATGAGCTCCATATGAGATTTCTTGGCATATTTTGGATTAATGACAGTTTGA 718
 QY 759 AAGCATCAAGCAAAATCACTTTTGAAGCAATCTGATGATGAGAGGATGACA 818
 DB 719 AAGCATCAAGCAAAATCACTTTTGAAGCAATCTGATGATGAGAGGATGACT 778
 QY 819 GCAAAAGTGAAGGCTGCTGCTTGGCTTCAATAGCGGCACTCTGATTTATCAAGT 878
 DB 779 GCTAAAGTGAAGGCTTCAATATGATGATGATGATGATGATGATGATGATGAT 838
 QY 879 GGTATGAAGATCGAGCATCTTAAAGTCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 938
 DB 839 GGTATGAAGATCGAGCATCTTAAAGTCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 898
 QY 939 CACAAGATGCAATTTTGGGATCATCTAAGATGATGATGATGATGATGATGATGAT 998
 DB 899 CACAAGATGCAATTTTGGGATCATCTAAGATGATGATGATGATGATGATGATGAT 958
 QY 999 GCGGAGAGGATTTTCAAGGATCAAGATTTGATCAAGAGAGGAGGAGGAGGAGGAG 1058
 DB 959 GCGGAGAGGATTTTCAAGGATCAAGATTTGATCAAGAGAGGAGGAGGAGGAGGAG 1018
 QY 1059 TTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
 DB 1019 TTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1078
 QY 1119 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1178
 DB 1079 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1138
 QY 1179 ATTAACCAAGAAAGATGACAGCTTGAAGATCTATCTGATGATGATGATGATGAT 1238
 DB 1139 ATTAACCAAGAAAGATGACAGCTTGAAGATCTATCTGATGATGATGATGATGAT 1180
 QY 1239 GACCTATTAACCAAGATCTTAAAGAGAGAGGTTGCTGATGATGATGATGATGATGAT 1298
 DB 1181 GATCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1240
 QY 1299 ACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1358
 DB 1241 ACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1300
 QY 1359 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1418
 DB 1301 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
 QY 1419 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1478
 DB 1361 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1420
 QY 1479 GGTGAAAACTATTTGCTTTTACACTAGATGATGATGATGATGATGATGATGATGAT 1538

DB 1421 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1480
 QY 1539 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1598
 DB 1481 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1540
 QY 1599 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1658
 DB 1541 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1600
 QY 1659 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1718
 DB 1601 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1660
 QY 1719 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1778
 DB 1661 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1720
 QY 1779 CTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1838
 DB 1721 CTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1780
 QY 1839 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1898
 DB 1781 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840
 QY 1899 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1958
 DB 1841 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900
 QY 1959 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1991
 DB 1901 GGTCAAACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1960
 QY 1992 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2051
 DB 1961 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2020
 QY 2052 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2111
 DB 2021 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2080
 QY 2112 ACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2171
 DB 2081 ACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2140
 QY 2172 ATCTGAG 2231
 DB 2141 ATCTGAG 2200
 QY 2232 AGTCTT 2237
 DB 2201 GACCTT 2206

RESULT 14
 US-10-424-599-44248/c
 ; Sequence 44248, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21 (53223) B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ. ID NOS: 285684
 ; SEQ ID NO 44248
 ; LENGTH: 2708

TYPE: DNA
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_139954C.1
 US-10-424-599-44248

Query Match 37.9%; Score 966.8; DB 12; Length 2708;
 Best Local Similarity 66.4%; Pred. No. 5.7e-260;
 Matches 1517; Conservative 0; Mismatches 617; Indels 150; Gaps 3;

96 GCCATGCGCAGCGCTCGACCCGTCGCCGAGCTTCGTAGGAGCAGTGAAGCGCTCATC 155
 Db GCCATGAGAACACAGATCTTGTAGACATTTCTCAAGAGTGTAAAGGCATCAATC 2574
 2633 GCCATGAGAACACAGATCTTGTAGACATTTCTCAAGAGTGTAAAGGCATCAATC 2574
 QY 156 AAGGTGGCAGCTGCACTGTTCTTCACAGCAAGATGGAAGTTGGCTTGGCGAGGTTGA 215
 Db AAGGTGGCAGCTGCTGTGTCACTGCGCAAGATGGAAGTTGGCTTGGCAAAATTAAGG 2514
 2573 AAGGTGGCAGCTGCTGTGTCACTGCGCAAGATGGAAGTTGGCTTGGCAAAATTAAGG 2514
 QY 216 GCTCTGCGAGCAGGTTAAGAACTGAACCTTTAGATACGAATGATTTTGGTCAAC 275
 Db GCACTCTGAGAGCATTAAGAGCTGAATCTCTTGTATGAGATTAATTTGGTGTCA 2454
 2513 GCACTCTGAGAGCATTAAGAGCTGAATCTCTTGTATGAGATTAATTTGGTGTCA 2454
 QY 276 TCAAGTGTGTTGAGTGGGCGACAGCACTTAGGTACCGAGCTTGTCAATAGCAC 335
 Db TCAAGTGTGTTGAGTGGGCGACAGCACTTAGGTACCGAGCTTGTCAATAGCACAGC 2394
 2453 TCAAGTGTGTTGAGTGGGCGACAGCACTTAGGTACCGAGCTTGTCAATAGCACAGC 2394
 QY 336 TTGCTGATCTGAAAAGCCAGATGAGTTAGTGAAGGCTTGTGCGCTGTGGT 395
 Db TTGCTGATCTTGAAGCCGCAAGTTGAATTTGATGAGAGGCTTGTGCTGTGGA 2334
 2393 TTGCTGATCTTGAAGCCGCAAGTTGAATTTGATGAGAGGCTTGTGCTGTGGA 2334
 QY 396 CAGAGTGAAGTGAAGTCTTTTACGATGTTTGAACCACTGAGTCTGTGATCT 455
 Db CAGAGTGAAGTGAAGTCTTTTACGATGTTTGAACCACTGAGTCTGTGATCT 2274
 2333 CAGAGTGAAGTGAAGTCTTTTACGATGTTTGAACCACTGAGTCTGTGATCT 2274
 QY 456 CAATCTTGTCTACCAAGATGTTTGAAGACCCAAAGTCCGGAGAGAACTCACTGA 515
 Db CAATCTTGTGTGAGCAATGATTTTGAAGACAAAGATTTCAAGTGAAGTCACTGAG 2214
 2273 CAATCTTGTGTGAGCAATGATTTTGAAGACAAAGATTTCAAGTGAAGTCACTGAG 2214
 QY 516 ACCTGTGAGTCAATTAAGTCTTAAAGTTATCAATATTTATGAAATGATGCAATC 575
 Db ACCTGTGAGTCAATTAAGTCTTAAAGTTATCAATATTTATGAAATGATGCAATC 2154
 2213 ACCTGTGAGTCAATTAAGTCTTAAAGTTATCAATATTTATGAAATGATGCAATC 2154
 QY 576 AGCATGGAAGGCTCCATATGAGATTCATCTGATATATCTGGATATATGACAGTTA 635
 Db AGCATGGAAGGCTCCATATGAGATTCATCTGATATATCTGGATATATGACAGTTA 2094
 2153 AGCATGGAAGGCTCCATATGAGATTCATCTGATATATCTGGATATATGACAGTTA 2094
 QY 636 GAGGAGCTGTGCACTGGAAGTGAAGTGAATCTCTATCTGCTCAGTGTGAT 695
 Db TCACTTATTTGGCATTTGAAATTAAGGATCTCTTATTTTGTGATGATGATGAG 2034
 2093 TCACTTATTTGGCATTTGAAATTAAGGATCTCTTATTTTGTGATGATGATGAG 2034
 QY 696 GAGGAGCTGTGCACTGGAAGTGAAGTGAATCTCTATCTGCTCAGTGTGAT 755
 Db GAGGAGCTGTGCACTGGAAGTGAAGTGAATCTCTATCTGCTCAGTGTGATGAG 1974
 2033 GAGGAGCTGTGCACTGGAAGTGAAGTGAATCTCTATCTGCTCAGTGTGATGAG 1974
 QY 756 GAAAGAGTCAAGCAAGAACTCACTTTGAGACAAATCTGCTAGTGAAGAGGAGCAT 815
 Db GAAAGAGTCAAGCAAGAACTCACTTTGAGACAAATCTGCTAGTGAAGAGGAGCAT 1914
 1973 GAAAGAGTCAAGCAAGAACTCACTTTGAGACAAATCTGCTAGTGAAGAGGAGCAT 1914
 QY 816 ACAGCAAAAGTGAAGGCTGCTGCTTGGCTTCAAAATGCGCACACCTGTGTTATTA 875
 Db ACTCTAAAGTGAAGGCTTCTATCATGAGCTGAAGCTGCACTCTGTATCATTAAT 1854
 1913 ACTCTAAAGTGAAGGCTTCTATCATGAGCTGAAGCTGCACTCTGTATCATTAAT 1854
 QY 876 ----- 875
 Db 1853 AGAATTTTAAATCAAGAACTATGAATTCATTTATGCTACCACTTTATGAG 1794
 876 -----AGTGGTTGAAT 890
 QY 1793 ATTTCATCTGCAAAATGTTTCTCTGTTCTGCAATTTAGTGTATGACAGCT 1734
 Db CGAGCATTTCTTAAGTTCTTCAAGGAAATTTGTATCTCTTTCAAGAGATGG 950
 891 CGAGCATTTCTTAAGTTCTTCAAGGAAATTTGTATCTCTTTCAAGAGATGG 950
 QY 1733 GAAATATCATTAAGTTCTTCAAGGAAATTTGTATCTCTTTCAAGAGATGG 1674
 Db

QY 951 AATTGTGGCAATCATTAAGATGTTAGTACTGCGAAGTGGCTTGGCCGAGAGAT 1010
 Db 1673 CATTAATGGGCCCCGGTAAAGAGGTTGATGCTCGAAGATGGCACTTCAGTGAAGGAC 1614
 QY 1011 TGTTCAGGATCTACAGAAATTTGTCATGAGAGGAAAGCAAAAGATATTTGCTAGATGT 1070
 Db 1613 TGTTCAGGATCTACAGAAATTTGTCATGAGAGGAAAGCAAAATTTTGTGCTAGATGT 1554
 QY 1071 GCGAGTCTTTGAGAGGCAATGAGATTTATATAGTCTGAGATGAGATGATGATGT 1130
 Db 1553 GCGAGTCTTTGAGAGGCAATGAGATTTATATAGTCTGAGATGAGATGATGATGT 1494
 1131 GCGAGTCTTTGAGAGGCAATGAGATTTATATAGTCTGAGATGAGATGATGATGT 1190
 Db 1493 GATGCAAAAGACAGATGATGAAATCTCTGTTGCTAGATCT----- 1450
 QY 1191 AAGATGCAAGCTTGCAGAAATCTATTCGTACCTTGCAGAAATGAGAGACCTTAATAC 1250
 Db 1449 -GCTTGCAGAGCTTGCAGAAATCTATTCGTACCTTGCAGAAATGAGAGACCTTAATAC 1392
 1449 -GCTTGCAGAGCTTGCAGAAATCTATTCGTACCTTGCAGAAATGAGAGACCTTAATAC 1392
 QY 1251 CAGATATCTTAAAGACAGAGGTTGCGATGATTTAGTCTTGAAGAAACATCTTCCCA 1310
 Db 1391 CAGATATCTTAAAGACAGAGGTTGCGATGATTTAGTCTTGAAGAAACATCTTCCCA 1332
 1391 CAGATATCTTAAAGACAGAGGTTGCGATGATTTAGTCTTGAAGAAACATCTTCCCA 1332
 QY 1311 TTAGGTTCTCTTAATTTTGTGATGCTCCGACCTGATGCTTGTGATGATGATCT 1370
 Db 1331 TTAGGATCTCTTTAATTTTGTGATGCTCCGACCTGATGCTTGTGATGATGATCT 1272
 1331 TTAGGATCTCTTTAATTTTGTGATGCTCCGACCTGATGCTTGTGATGATGATCT 1272
 QY 1371 TTGCGATTTGGAAGTGTATGCTCTTCCCTTAAAGGTTGAAAGAGATCAGATCA 1430
 Db 1271 TTGCGATTTGGAAGTGTATGCTCTTCCCTTAAAGGTTGAAAGAGATCAGATCA 1212
 1271 TTGCGATTTGGAAGTGTATGCTCTTCCCTTAAAGGTTGAAAGAGATCAGATCA 1212
 QY 1431 AACAGATTTGCAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1490
 Db 1211 AATGCAATTTGCAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1152
 1211 AATGCAATTTGCAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1152
 QY 1491 ATTGGCTTTGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1550
 Db 1151 ATTGGCTTTGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1092
 1151 ATTGGCTTTGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1092
 QY 1551 GATCTGTCTCTCAAGAGGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1610
 Db 1091 GATCTGTCTCTCAAGAGGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1032
 1091 GATCTGTCTCTCAAGAGGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1032
 QY 1611 ATTCTGTTCTTGGCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1670
 Db 1031 ATTCTGTTCTTGGCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 972
 1031 ATTCTGTTCTTGGCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 972
 QY 1671 ATGATATGCGAAATCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1730
 Db 971 CTGAGATGCGAAAGGCGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 912
 971 CTGAGATGCGAAAGGCGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 912
 QY 1731 GCAATGAGACCTTACTAGTTCATTAAGATCTTATGAGAGTCCAGGCTTGAAGACATA 1790
 Db 911 GCAATGAGACCTTCTTGTGTTCAAGAGACCTTGTGAGAGAGGCTTGAAGATAT 852
 911 GCAATGAGACCTTCTTGTGTTCAAGAGACCTTGTGAGAGAGGCTTGAAGATAT 852
 QY 1791 TTAAGTACCTAATAAGAGAGGATTAATTTATGAGGACCTTATGCGCAAAAGCT 1850
 Db 851 ATTAATGACCTAATAAGAGAGGATTAATTTATGAGGACCTTATGCGCAAAAGCT 792
 851 ATTAATGACCTAATAAGAGAGGATTAATTTATGAGGACCTTATGCGCAAAAGCT 792
 QY 1851 CTGGATTTCCAAAGCTGTTTCAATTCATGATGATGATGATGATGATGATGATGATGAT 1910
 Db 791 TTAATATTCAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
 791 TTAATATTCAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
 QY 1911 GAGTTTGTATGATGTTTCAATGAGCAATGACATTTGATGATGATGATGATGATGAT 1963
 Db 731 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
 731 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
 QY 1964 -----TGTCTATACAGATTTGATGATGATGATGATGATGATGATGATGATGAT 2003
 Db 671 ACTCTTATTTCTGATATTTGACATATGATGATGATGATGATGATGATGATGATGATGAT 612
 671 ACTCTTATTTCTGATATTTGACATATGATGATGATGATGATGATGATGATGATGATGAT 612

28	46.6	1.8	1830121	4	US-09-643-990A-1	Sequence 1, Applt
29	43.8	1.7	1656	4	US-09-446-301A-1	Sequence 1, Applt
30	43.8	1.7	1656	4	US-09-446-301A-1	Sequence 1, Applt
31	43.8	1.7	2411	4	US-09-446-301A-15	Sequence 15, Applt
32	43.8	1.7	2411	4	US-09-446-301A-15	Sequence 15, Applt
33	42.8	1.7	1125	2	US-08-709-874A-25	Sequence 25, Applt
34	42.8	1.7	1125	2	US-09-104-874A-25	Sequence 25, Applt
35	42.8	1.7	1125	4	US-09-833-555-25	Sequence 25, Applt
36	42.6	1.7	29555	4	US-08-956-171B-206	Sequence 206, App
37	42.2	1.7	819	4	US-09-107-532A-944	Sequence 944, App
38	41.6	1.6	832	4	US-09-621-976-2813	Sequence 2813, App
39	38.8	1.5	1584	4	US-09-328-352-775	Sequence 775, App
40	38.2	1.5	1149	4	US-09-328-352-355	Sequence 355, App
41	38	1.5	357	4	US-09-775-932-23	Sequence 23, Applt
42	38	1.5	20199	4	US-08-961-527-6	Sequence 6, Applt
43	37.8	1.5	580073	4	US-08-545-528D-1	Sequence 1, Applt
44	37.2	1.5	480	4	US-09-134-000C-1373	Sequence 1373, App
45	37	1.5	640681	4	US-09-790-988-1	Sequence 1, Applt

ALIGNMENTS

RESULT 1
US-07-953-695A-1
Sequence 1, Application US/07953695A
Patent No. 5344923
GENERAL INFORMATION:
APPLICANT: VERRA, D. et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding For Bifunctional Enzymes For Procl
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kremblae, Foster, and Millard
STREET: 7632 Slate Ridge Blvd.
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43068
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/953, 695A
FILING DATE: 19920929
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foster, Frank H.
REGISTRATION NUMBER: 24,560
REFERENCE/DOCKET NUMBER: URF 2-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 575-2100
TELEFAX: (614) 575-2149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2417 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: CDNA
DESCRIPTION: Sequence encodes Pyrroline-5-carboxylate synthetase, a bifunctional
FRAGMENT TYPE: N-terminus: N-MESAVDPS--C-terminus: ---RRRGMN-C
FRAGMENT TYPE: Internal Fragment: --VDAREMAY--
ORGANISM: Vigna aconitifolia
STRAIN: Mottbean
DEVELOPMENTAL STAGE: Root nodules
IMMEDIATE SOURCE:

LIBRARY: cDNA expression library
 CLONE: cDNA clone
 PUBLICATION INFORMATION:
 AUTHORS: Chien-An A. Hu, Ashton J. Delaney and Desh Pal S. Verma
 TITLE: A bifunctional enzyme (deltaal-pyrroline-5-carboxylase synthetase) catalyz
 JOURNAL: Proceedings of the National Academy of Science USA
 VOLUME: 89
 ISSUE: October
 PAGES: 9354-9358
 DATE: OCT-1992
 RELEVANT RESIDUES IN SEQ ID NO: 1: FROM position 37 to position 2049 Genbank M
 US-07-953-695A-1

Query Match 42.9% Score 1092.8; DB 1; Length 2417;
 Best Local Similarity 70.9%; Pred. No. 5.5e-312;
 Matches 1519; Conservative 0; Mismatches 617; Indels 6; Gaps 5;

108 GTGACCCGTCGAGCTTGTGAGGAGCGGCTCATCATCAAGTGGGACCT 167
 49 GTGATCTCTCCGGGGTTCATAGAGCGTGAAGCTGTGATCATCAAGTGGGACCT 108
 168 GCAGTGTCTCCAGACAGATGAAAGTGGCTTTGGGAGGGTGGAGCTGTGGAG 227
 109 GCGGTGTCTCTCGAAGAGAGAGGTAGCGGTGGAAGATTGGAGCTCTGTGGAG 168
 228 CAGGTTAAGAACTGAATCTTTAGATACGAGTGAATTTGTGTCACCTGAGTGTCT 287
 169 CAGATTAGCAACTCACTCTCGAATACGATTAATACCTGCTCTCGGCCCCGTC 228
 288 GAGGTGGGGGCGACAGCACTTAGTACCGGAGAGCTTGTCAATAGACCTTGTGATCTG 347
 229 GGTATGAGCGCCAAAGGCTACGTTCCGTAAATTAATCAACAGCACTTGTGCGACCTT 288
 348 CAAAGCCAGAGATGAGTATGATGAAAGGCTGTGCGGCTGTGTGTCAGATGAGCTG 407
 289 CAGAAACCCCACTGAGCTGAGCGGAGAGGCTGCGGCGGCTGAGACAGAAAGCTCTC 348
 408 ATGCTCTTTACGATATGTTGTTAACCAGTGTCTGTGATCTCACTTCTTGTGTC 467
 349 ATGCTCTCTACGATACGCTGTCACTGATGATGATGATGATGATGATGATGATGATG 408
 468 ACCGAGTGAATTTGAGAACCCAAAGTTCGGGAGCACTCACTGAACTGTGAGTCA 527
 409 ACGGTAACGATTTTCGAGTAAGATTTTCAGGAAGCACTTACGAGCTGTGAGTCTG 468
 528 TTATTAATCTTAAGTTAATCAATATTTAATGAAATGATGATGATGATGATGATGATG 587
 469 CTGTTGGCGTGAAGTTATCCGGTGTTCATGATGAGAGCATGCGCTTATGATGATGATG 528
 588 GCTCATATGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 647
 529 GCTCCCTATGAGATTTCTGTGATATTTTGGATGATGATGATGATGATGATGATGATG 588
 648 GCATGGAATGAAAGTATCTCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
 589 GCTTGAAGTTAAAGCCGATCTCTTGTGTTGATGATGATGATGATGATGATGATGATG 648
 708 GGTCCACCAAGTGAACATCATCAAAATCATACACTTATTTAATGAAAGAAAGCATGAG 767
 649 GGCCTCCCAAGTGAACCTTCATCAAGCTTATTTATCATATTAACAAAGAAAGAAAGCATG 708
 768 CAAAGAAATCACTTTGAGAGAAATCTGCTGATGATGATGATGATGATGATGATGATGATG 827
 709 AATGAATTAATCTTTGGGAGCAAGCTGATGATGATGATGATGATGATGATGATGATGATG 768
 828 AAGGCTGTCTTTGGGCTTCAAAATGAGGACACTGTGTGTTATTTAACAAGTGGTGGTGA 887
 769 AAGGCTGTCTTTGGGCTTCAAAATGAGGACACTGTGTGTTATTTAACAAGTGGTGGTGA 828
 888 AATGAGAGATTTTAAAGTCTTCTATGAGGAGAAATTTGATGATGATGATGATGATGATG 947
 829 CCGTGAATATATCATTAATGTTCTCCAGAGCAAGCTATAGGAATCTCTTCTCATTAAGAT 888

948 GCGAATTTGGGAAATCATTAAGGATGTAGTACTGCTGATGATGATGATGATGATGATGATG 1007
 889 GCGATGAGTGGGCTCAAGTAAAGAGTTATGATGATGATGATGATGATGATGATGATGATG 947
 1008 GATGTTCAAGGATCTCAAGATTTTGTATGAGAG-ACGAAAGAAAGATTTGCTTGA 1066
 948 GATGTTCAAGGATCTCAAGGATTTATCTTCAAGGAAAGAAAGAAATTTTACTTAA 1007
 1067 TGTTCAGATGCTTTGGAGGCAATGAGATTTAATGATGATGATGATGATGATGATGATGATG 1126
 1008 AATG 1067
 1127 AGCTCGGCCCCAGTGTGTGATGATGAGAGCTTTGTGCTGATGATGATGATGATGATGATG 1186
 1068 TACTGCTGCAAGAAAGAGGATGATGAAATTCCTGTGTGCTAGGCTTATTAAC 1127
 1187 AGGAAGATGAGAGCTTTGCAAAATCTATTGATGATGATGATGATGATGATGATGATGATG 1246
 1128 TGGGAAGATGAGAGCTTTGCAAAACATGATGATGATGATGATGATGATGATGATGATG 1187
 1247 AAGCAGATCTTAAAGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1306
 1188 TGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1247
 1307 CCGATTAAGTGTCTTAAATTTTGTGATGATGATGATGATGATGATGATGATGATGATG 1386
 1248 TCCCTTGGAGAGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1307
 1367 ATCTTGGCAATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1426
 1308 TTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1367
 1427 ATCAACAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1486
 1368 ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1427
 1487 ACTTATGAGCTTTTAAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1546
 1428 ACTTATGAGCTTTGAGCTCTCAAGGAGAGATGATGATGATGATGATGATGATGATGATGATG 1487
 1547 CATTAATCTTGTCACTGCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1606
 1607 TAAAGTCTGCTTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1666
 1548 TAAATTTCTGTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1607
 1667 TGAATG 1726
 1608 TAACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1667
 1727 CAATG 1786
 1668 CAATG 1727
 1787 CATATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1846
 1728 GATCATTTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1787
 1847 AGCTGTGAGATTTCAAAAGCTTTTCAATCATGATGATGATGATGATGATGATGATGATGATG 1906
 1788 TGTGTTAATTAATTTCAAGAGCAATTTATCATGATGATGATGATGATGATGATGATGATGATG 1847
 1907 TGTGATG 1966
 1848 CCGCAATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1907
 1967 TCAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2026
 1908 ACAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1967
 2027 TGAATG 2085

DB 1968 AGACAGTCTGCTGTTTTCATCAATGACACCAAGTTAGTACGCGGACGATTGA 2027
CY 2086 GATTGGTGTGAGTTGGATAGACACAGGGGCTATCCATGCCGTGACCAAGTGGTG 2145
DB 2028 GACTAGGCGGAGAGTTGGAATTATGATCAAGACGATTCATGCTCGAGGTCAAGTAG--A 2085
CY 2146 TTGAAGTCTCTTACTACACGATGATCTTGGAGAGACTGGCAAGTGTGAATGTG 2205
DB 2086 GTTAGGATTTGTTAACAACAGATGATCTAAAGGAAAG--GACACAGTGTGATGTG 2144
CY 2206 ACAAGATGTCTGTACACCAATAGAGTCTCTTTCGAAT 2247
DB 2145 ATAGAGGCGTTGTCTACACCAACCAAGCTTGCAATTAT 2186

RESULT 2
US-08-267-259-1
Sequence 1, Application US/08267259
Patent No. 5639950
GENERAL INFORMATION:
APPLICANT: VERMA, D. et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding For Bifunctional Enzymes For Pro
Patent No. 5639950
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Krenblas, Foster, and Willard
STREET: 7632 Slate Ridge Blvd.
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43068
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,259
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/953,695
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Foster, Frank H.
REGISTRATION NUMBER: 24,560
REFERENCE/DOCKET NUMBER: URF 2-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 575-2149
FAX: (614) 575-2149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: Sequence encodes Pyrroline-5-carboxylate synthetase, a bifunctional
Patent No. 5639950
FRAGMENT TYPE: N-terminus: N-MESAVDPS--
FRAGMENT TYPE: C-terminus: --RRRGM--C
FRAGMENT TYPE: Internal Fragment: --VDAREMAV--
ORIGINAL SOURCE:
ORGANISM: Vigna acuminatifolia
STRAIN: Mothbean
DEVELOPMENTAL STAGE: Root nodules
IMMEDIATE SOURCE:
LIBRARY: cDNA expression library
CLONE: cDNA clone
PUBLICATION INFORMATION:
AUTHORS: Chien-An A. Hu, Ashton J. Delaney and Desh Pal S. Verma
TITLE: A bifunctional enzyme (deltaal-pyrroline-5-carboxylate synthetase) catalyz

JOURNAL: Proceeding of the National Academy of Science USA
VOLUME: 89
ISSUE: October
PAGES: 9354-9358
DATE: OCT-1992
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM position 37 to position 2049 GenBank
US-08-267-259-1

Query Match 42.9% Score 1092.8; DB 1; Length 2417;
Best Local Similarity 70.9% Pred. No. 5.5e-312;
Matches 1519; Conservative 0; Mismatches 617; Indels 6; Gaps 5;

DB 108 GTCCAGCCGTCCTCCGAGCTTGTGAGGAGCGTGAAGCGCTCATCATCAAGTGGGACT 167
CY 49 GTGATCTTCTCCGGGGTTATGAGGAGGTGAAGGTGTGATCATCAAGTGGGACC 108
DB 168 GCAATGTTCTTCAAGCAAGATGAAAGTTGGCTTTGGCAGGGTTGAGACTCTGTGGAG 227
CY 109 GCGGTGTCTACTCGCAAGAGGAGGTGACCGGTGGAAGATTGGAGAGCTGTGGCAG 168
DB 228 CAGTTTAAAGAACTGAATCTTTTGAATAGAGATTTTGTGTCACCTCAGTGTGT 287
CY 169 CAGATTAGCACTCACTCTCTCGATACACATTATCTGCTCTCTGCGCCCTC 228
DB 288 GCAATGGGCGGCAAGCAGCTTAGGTACCGGAGCTTGTCAATAGCACTTGTGATCTG 347
CY 229 GGTATTGACCGCAAGGCTAGTTCCGTAAATTAACAACAGACTTCCGACCTT 288
DB 348 CAAAGCCACAGATGATTTAGTGAAGGCTGTGCGCGTGTGTGAGAGTGA 407
CY 289 CAGAAACCCCAACTGAACTGACGCGAGGCTGCGCGCGTGTGACAAACAGTCTC 348
DB 408 ATGCTCTTTAAGATGATGTTTAAACCACTGATGTCTGATCTCACTTCTTGTG 467
CY 349 ATGCTCTTAAGATGATGTTTAAACCACTGATGTCTGATCTCACTTCTTGTG 408
DB 468 ACCGACATGATTTTGAAGAACCCAAAGTTCGGGAGCACTCATGAACTGTGATCA 527
CY 409 ACGGATTAACGATTTTGAAGATTTGAGAGGCTTCTGAGCTGTGAAGTGC 468
DB 528 TTATTAGATCTTAAGATTAACCAATTTATGAAATGATGACATCAGACTAGAAG 587
CY 469 CTGTTGGCGCTGAAGTTATTCGGGTTCATGAGAACATGCGTTAGTACCAGAG 528
DB 588 GCTCCATATGAGATTCATGATGATTTTGAAGTTCGGGATTAAGACGTTTGAAGTGTG 647
CY 529 GCTCCATATGAGATTCATGATGATTTTGAAGTTCGGGATTAAGTGTGATTTTGA 588
DB 648 GCACTGGAAGTGAAGCTGATCTCTTATCTGCTGATGATGAGTGGTGTGATGT 707
CY 589 GCTTGGAGTTAAGGCGGATCTCTGTTTGTGATGATGATGAGTGGTGTGATGT 648
DB 708 GGTCCACCAAGTGAACCATCATCAAAATCATACACTTATTAAGAAAGATCAG 767
CY 649 GGCCTTCAAGTGAACCTCATTAAGCTTATTAATATCAATTAACAAAGAAACATAG 708
DB 768 CAAAGATCATCTTTGAGACAAATCTGTGTAGTGAAGAGCATACGCAAAAGT 827
CY 709 ATGAAATTAATCTTTGGGACAGCTGAGTGGGAAAGGCGGAAATACCTGCAAGT 768
DB 828 AAGCTGTGCTTGGCTTCAATATGACGCAACCTGTGTTATTAACAGTGGTTTGA 887
CY 769 AAGCTGTGCTTCAATATGACGCAACCTGTGTTATTAACAGTGGTTTGA 828
DB 888 AATCGAGATCTTTAAAGTCTTTCATGAGGAAAAAATGATCTCTTTCACAAAGAT 947
CY 829 CCTGAAATATCATTAAGTCTTCCAAAGACACGTATAGAACTCTTTCATTAAGAT 888
DB 948 GCAATTTGTGGGAATCATTAAGATGTTAGTACTCGTGAATGCTGTGTCCGCAAG 1007
CY 889 GCACATGAGTGGCGCAAGTAAAGAGTTATGACGTGAGAGGCTGTGAGGC--AGG 947
DB 1008 GATTGTTCAAGGATCTCAAGATTTGTATCAAGAG--AACGAAAAAAGATTTGCTAGA 1066

Db 948 GAAATGTCAGAAAGCTCCAGGCTTATCTTACAGAGAAAGAAATTTTACTTAA 1007
 Qy 1067 TGTTCAGATGCTTTGGAGGCAATGAGATTTTAAAGCTTGAAGTGAAGTGT 1126
 Db 1008 AATAGCTGATGCTTGAAGCAATGAAATTAATCAAGATTGAATGAAGCTGATGT 1067
 Qy 1127 AGCTGGGCGCAAGTGTGTGATGAGAGAGCTTTGTGTGATGATGATTAATACC 1186
 Db 1068 TACTGTGACAAAGAGAGATGAAATATCTTGGGCTAGGCTTAAATACC 1127
 Qy 1187 AGGAAGATAGCAAGCTTGCATAATCTATTCCTTGCATAATGAGAGCTTAT 1246
 Db 1128 TGGGAAGATGCAAGCTTGCATAATGAGAGATGCAATGCAATGAGAGATCCAT 1187
 Qy 1247 AAACCGATATCTTAAAGAGAGAGTGTCTGATGATTTAGTCTTGAAGAAATCTTG 1306
 Db 1188 TGGTCAGATTTAAACGATCCAGAGCTTCAATGGGCTAATTTTGAAGAGCATATC 1247
 Qy 1307 CCATTAAGTGTCTCTTAAATGTTTGTAGTCCGAGCTGATGCTTGTGATGATGTC 1366
 Db 1248 TCTTTGGAGTGTCTCTTATTTTGTAGTCAAGTCTGATGCTTGTGATGATGTC 1307
 Qy 1367 ATCTTTGGCAATTCGAGTGTGATGATGCTTCTTAAAGGTGAAAGAGCTATCAG 1426
 Db 1308 TTCAATGGCAATCCGAGTGTGATGATGCTTCTTAAAGGTGAAAGAGCTATCAG 1367
 Qy 1427 ATCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1486
 Db 1368 ATCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1427
 Qy 1487 ACTTATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1546
 Db 1428 ACTTATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1487
 Qy 1547 CATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1606
 Db 1488 AATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1547
 Qy 1607 TAAGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1666
 Db 1548 TAAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1607
 Qy 1667 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1726
 Db 1608 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1667
 Qy 1727 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1786
 Db 1668 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1727
 Qy 1787 CATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1846
 Db 1728 GATCATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1787
 Qy 1847 AGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1906
 Db 1788 TCTGTTAAATTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1847
 Qy 1907 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1966
 Db 1848 CGCCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1907
 Qy 1967 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2026
 Db 1908 ACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1967
 Qy 2027 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2085
 Db 1968 AGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2027
 Qy 2086 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2145

Db 2028 GACTAGGCGAGAGCTTGAATTTAGTACAGAGAGATTCATGCTCAGAGTCAATAG--A 2085
 Qy 2146 TTGAAGCTCTTAACTTACACAGATGATGATGATGATGATGATGATGATGATGATG 2205
 Db 2086 GTTGAAGATGTTTAAACAGAGAGATGATGATGATGATGATGATGATGATGATG 2144
 Qy 2206 ACAAGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2247
 Db 2145 ATGAGGCGTGTCTACACAGAGATGATGATGATGATGATGATGATGATGATGATG 2186

RESULT 3
 US-09-313-294A-4491
 ; Sequence 4491, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Laljudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ. ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ. ID NO. 4491
 ; LENGTH: 291
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Inocyte ID No. 6476212 700348515H1
 ; LOCATION: 205
 ; NAME/KEY: 205
 ; OTHER INFORMATION: a, t, c, g, or other
 ; US-09-313-294A-4491

Query Match 7.5%; Score 190.6; DB 4; Length 291;
 Best Local Similarity 80.7%; Pred. No. 2.9e-46;
 Matches 234; Conservative 0; Mismatches 55; Indels 1; Gaps 1;

Qy 705 AGTGTCCACCAAGTGAACCATCATCAAAATCATACACATTAATTAAGAAAGCAT 764
 Db 2 AGCGTCCACCAAGTGAACCATCATCAAAATCATACACATTAATTAAGAAAGCAT 61
 Qy 765 CAGCAAAATCACTTTTGAAGCAAAATCTCGTGTGATGATGATGATGATGATGATG 824
 Db 62 TACAGTGAATTAATTTTGGGATTAAGTCACTGTGATGATGATGATGATGATGATG 121
 Qy 825 GTGAAGCTGTGCTTGTGCTTCAAAATGAGGAGCACTGTGTGATTAACAGTGGATT 884
 Db 122 GTGAAGCTGTGCTTGTGCTTGAACAGTGGAGCACTGTGTGATTAACAGTGGATT 181
 Qy 885 GAAATGAGAGATCTTAAAGTT-CTTATGGGAGAAATTTGTTACTCTTTACAA 943
 Db 182 GCATCTCAGAGCAATTTTGAAGTCCCAAGAGAGAAATTTGTTACTCTTTACAA 241
 Qy 944 GAATGCAATTTTGGAGATCATCTAAGATGTTAAGTCTGTGATG 993
 Db 242 GATGCAAGTCTGTGGAGCAATCCAGAGATTTAAGTCTGTGATG 291

RESULT 4
 US-09-313-294A-1035
 ; Sequence 1035, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Laljudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 7600
 SOFTWARE: PERL Program
 SEQ ID NO 1035
 LENGTH: 276
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. 6476212 700550271H1
 LOCATION: 6, 28, 56, 118, 144, 182, 237, 245, 256
 OTHER INFORMATION: a, t, c, g, or other
 US-09-313-294A-1035

Query Match 7.2%; Score 183; DB 4; Length 276;
 Best Local Similarity 80.4%; Pred. No. 4.9e-44;
 Matches 221; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

Qy 574 TCACACACTAGAAAGGCTCATATAGAGTTCATCTGTATATTCCTGGATATATGACAGTT 633
 Db 1 TCACACCTAGAAAGGCTCATATAGAGTTCATCTGTATATTCCTGGATATATGAGAGTT 60
 Qy 634 TAGCAGACTGTGGCTGCTGAACTGAAAGCTGATCTCTTATTTCTGCTGAGTATG 633
 Db 61 TAGCTGTCTTTTGGCTATTTGAACTTAAAGCAGATCTCTGTTCTTCTAAGATGATGAG 120
 Qy 694 ATGGCTGTATATAGTGTCCACCA-AGTGAACCATCATCAAAATCATACACTTATTT 752
 Db 121 ATGGCTGTATACAGGCTGTCCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
 Qy 753 AAGAAAGCATCAGCAAGAAATCACTTTTGGAGCAAAATCTGCTAGAGTAAAGAGGC 812
 Db 181 AAGAGTAAACATTAAGTGAATTAATTTTGGAGTAAAGTCACTGAGTAAAGAGGAGG 240
 Qy 813 ATGACGCAAAAGTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847
 Db 241 ATGAAAGCTAAAGTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 275

RESULT 5
 US-09-543-681A-1122
 Sequence 1122, Application US/09543681A
 Patent No. 6665709
 GENERAL INFORMATION:
 APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 FILE REFERENCE: 2709.1002-001
 CURRENT APPLICATION NUMBER: US/09/543,681A
 CURRENT FILING DATE: 2000-04-05
 PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 8344
 SEQ ID NO 1122
 LENGTH: 1281
 TYPE: DNA
 ORGANISM: Proteus mirabilis
 US-09-543-681A-1122

Query Match 6.9%; Score 175.4; DB 4; Length 1281;
 Best Local Similarity 48.6%; Pred. No. 2.4e-41;
 Matches 590; Conservative 0; Mismatches 596; Indels 27; Gaps 3;

Qy 988 AATAGCTCTTCCCGCAGAGTGTTCAGGCACTACAGAAATTTGTCACAGAGAAC 1047
 Db 38 AATAGGAAAAGCGCGCGAGAGGCTTCTTGGCACTTACCTACCTATCAACCGAACHAA 97
 Qy 1048 GAAAAAAGATATTGCTAGATGTTGAGATGCTTTGAGAGCAATAGAGATTAAAGT 1107
 Db 98 AAAATCAGGCACTGTATGATCGCTGATTTATTGAACAAGCAAGAACCAATTTCTTG 157
 Qy 1108 CTGAGATGAGAGCTGATGCTGCGGCCCAAGTTGCTGATATGAGAGGCTTTGGTTG 1167

Db 158 CTGTAATGAAAAGATATGATGCGGCGACGAGAGTCTAATATTAATGCTCAATGCTTG 217
 Qy 1168 CTAGATGACTATTAACCAAGAAAAGATAGCAAGCTTGCAGAAATCTATTCGACCTTG 1227
 Db 218 ATCGTTTATTACTCATCAGAGGCTTTAAAGGAGCTGATGATGATGATGATGATGATG 277
 Qy 1228 CAATATGAGAGACCTTAAACAGATATCTTAAAGACAGAGGTTGCTGATGATTTAG 1287
 Db 278 GTGATCTAGAGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 337
 Qy 1288 TTCTTGAGAAAACATCTTCCCATTTAGGTTCTTCTTATTTGTTTGAATCCGACCTG 1347
 Db 338 GTTTAGAACGCCGCCGAGTCCCTTTAGGGGTGTTGGGCTTATTTAAGCAAGCTGCTCA 397
 Qy 1348 ATGCTTGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
 Db 398 ATGTGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457
 Qy 1408 GTGAAAAGAGCTATCAGATCAACAGATATGATGATGATGATGATGATGATGATGATG 1458
 Db 458 GCGAAAAGAGCTACCACTAATCAAGCGGTTGCGGCTGATCCAGAGAGCTAG 517
 Qy 1459 ATGCTATTCCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1518
 Db 518 AAACATGCTATTCCTGCGCTGCTATTAAGCTATGATGATGATGATGATGATGATGATG 577
 Qy 1519 TCGCAGATTTGCTAAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1578
 Db 578 TCGCAAAAATGCTAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 637
 Qy 1579 AGCTGTCTCTCAATCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1638
 Db 638 GATTAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 697
 Qy 1639 TANGCAGCTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1698
 Db 698 TTGTTCACACCTTGTGTGAGAAAGTGTGATTTAGCAAGCATTAATGATATATTA 757
 Qy 1699 ATGCAAAAATGATTAACCGAGGCTGATGATGATGATGATGATGATGATGATGATGATG 1758
 Db 758 ATGCTAAAGTCAAGGCTCCAGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 817
 Qy 1759 ATCTATGAGAGGCTCAGGCTTAC-----GACATATGATGATGATGATGATGATGAT 1812
 Db 818 CTATTCGCGAGGATTTCTTGCCTCAATTAAGATGCGATGCGACACAAAAGTACT 877
 Qy 1813 GAGTTAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
 Db 878 TGATGCGAGTCAAGCGCTATATGATGATGATGATGATGATGATGATGATGATGATGATG 937
 Qy 1861 CAAGAGCTTTTCAATTTATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
 Db 938 TGCAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 997
 Qy 1921 ATGATGCTCAATCAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
 Db 998 ATGATTTAAGGCGGCAATGCTCATATTCGCAATATGATGATGATGATGATGATGATG 1057
 Qy 1981 TCGTCTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
 Db 1058 TTTTAAAGCAATCTATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1117
 Qy 2041 TATTATATGAGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
 Db 1118 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1177
 Qy 2101 TTGCAATAGCAAGGCGGATTCATGCGCGTGAACAGTGGGTGTTGAAGTCTTTA 2160
 Db 1178 TACCGGTGATCACAAAAAGCTACATGACAGAGGCGCTTATGAGATTAATGATGCTTAC 1237
 Qy 2161 CTACAGATGAT 2173

DB 707 GTCAATGTTGTAGAGACACAGCGACTTACAAAAGGTTACCAATTACCTTGATG 766
CY 1702 CAAAACCTGATTACCCAGAGCCTGCAATGATGAGACCTTACTATGTTCAATGAGATC 1761
DB 767 CTAAGACACATCGTTACGGCGTTTGTATGCAATGGAAGAACTGCTGCTGTGAAGAAAA 826
CY 1762 TTAAGAGAGT-----CCAGGCTTACACGACATATAGTAGCACTAAAACAGA---AG 1812
DB 827 TTGCAGAGATTTTCTTACACACATGCTGAGCTTTATGCTGAAAAACAGATTGAGTAC 886
CY 1813 GAGTAAATATTATGTGAGGACCTTATGCGACAAAGCTCTGGGATTTCCAAAAGCTGTTT 1872
DB 887 GTGTGTCGCCAGAAACAGTGTATTTTAGAGAACTCTGTAACCTGCCACAGAGAGAG 946
CY 1873 CATTTCAATGATGATATGTTCTATGCGCTGCACTGTGAGTTGTTGATGATGTTCAAT 1932
DB 947 ATTGTATACCGAATATTAGAGCCGATCTTGCAATTTAAAGTGTAGCGGATTTGATG 1006
CY 1933 CAGCAATTGACCAATTCATGCTTATGGAAGTGTCTCATACAGATTGTATGCACTACAG 1992
DB 1007 AAGCAATTGACCAATTCATCAAAATATGTTGTCATACATGCAATGCTATGTGACAGAG 1066
CY 1993 ATGATAGGTAGAGAGACTTTTCTACAGAGATTGATAGTGTCTGTATTTCAATATG 2052
DB 1067 ACTATACCTTGGCAGCTGATCTTGCTGCTGCGATGATCAAGCTCCGTGTAGTTAATG 1126
CY 2053 CAAGACAGAGATTCCTGATGAGGCTGTTTGGATTGGGTGCTGAGATGGCACTAAGCA 2112
DB 1127 CATCACTCGTTTGGCGATGCTTGAATATGTTTAGTGTCTGGAATTTGATCTCAA 1186
CY 2113 CAGGCGATTCATGCGCGTGAACCAAGTGGTGTGAGGTCTCTTAATCACTACAGATGA 2172
DB 1187 CAGATTAAGATTCATGACGCGCGCTGTGTGCTTAGAAGTTTAACCTTCAAAAAATGGA 1246
CY 2173 TGTGCGAGGAGCGTGGGCACT 2194
DB 1247 TTGTTTAGTGTAGCGGTCAAT 1268

RESULT 9
US-09-557-884-1/c

Sequence 1, Application US/09557884

Patent No. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments

Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 4.9%; Score 125.8; DB 4; Length 1830121;
Best Local Similarity 45.9%; Pred. No. 1.2e-24;
Matches 537; Conservative 0; Mismatches 607; Indels 27; Gaps 2;

CY 1039 CAGAGGAGCAAAAAGATTTGCTAGATGTTGAGATGCTTTGGAGCAATGAGATT 1098
DB 1312952 CTGCTGAAAAAATTTGCTATTCATTTATTTGCAAGAACCTGACAAACAGACCGC 1312893
CY 1099 TAATAAGCTGTGAGATGAGCTGATGAGTGGCGCCCAAGTTGCTGATATGAGAAC 1158
DB 1312892 TTATCTTAGCCGAAAAACGCAAAAGATTTGAATCTGCCAACAATGATATGAGATG 1312833
CY 1159 CTTTGGTCTGATTTGATGATTAACCAAGAAAGATGCAAGCTTGCATAATCTATTC 1218
DB 1312832 CTTGATTTGATGCTTACTGCTACACAAAGACGTTTACAAAGGATGCTATGATGATC 1312773
CY 1219 GTACCTTGCATAATTTGAGAAAGCCTTATTAACAGATCTTAAAAAGACAGAGTTGCTG 1278
DB 1312772 GCCAGATTATTTCTTACAGATATCCCGGGGAAAAATCATAGAGCGGCTACATGATA 1312713
CY 1279 ATGATTTAGTTCTTGAAGAAACATCTTCCCATTTAGTGTCTCTTAATTTGTTGAGT 1338
DB 1312712 GCGGACTTAAATTCAGACGCGTACGACTCCGCTAGGGGTCAATGTTATATGAG 1312653
CY 1339 CCGAGCTGATGCTCTGTTGATGATTTGATGCTTTGGCAATTGAAAGTGTATGCTTTC 1398
DB 1312652 CTGGCCCAATTTAACATTTATGAGGCAAGCTTTTGCCTTAAACGGGTATGACGTA 1312593
CY 1399 TCTTAAAGTGTGAAAGAGAGCTATCAGATCAACACAGATTTGATAGTTATACCTG 1458
DB 1312592 TTTTACGGCGTGTGTAAGAAACAGATTTTCTTAAACAGATTTTAAAGTTGCAAA 1312533
CY 1459 ATGCTATTCCTGTATGTTGTGTAAGAACTTATTTGGC-----TTGTTTACATCA 1509
DB 1312532 ATGCTTTAGAGAGACAGGCTTACCAAAATTTGCGGTCAAGCATTAACGATCCAAAC 1312473
CY 1510 GAGATGAGATCGCAATTTGCTAAAGCTTGAATGATGATGATCTTGTCACTCCAAAG 1569
DB 1312472 GTGAAGCTGTATGCAATTTAAAGTGAATGATGATGATTTATTTCTCGTG 1312413
CY 1570 GAAATTAAGCTTGTCTCTCAATCAAGGCGTCACTTAAGATTTCTTGTGGCATG 1629
DB 1312412 GTGGTTCCGGTTTACATGATTTGTGTAACCAATTCGACTATTTCTTATTTGGGGTG 1312353
CY 1630 CTGATGTTATGCAACGATATATATTTGACAAATCAGTGAAGTATGCAAAACTTA 1689
DB 1312352 GTGTGGGTTTTGTATCTTACTTGTGAAAAAGTCGGAATTAAGATTTTGTG 1312293
CY 1690 TTGTAATGATGCAAAAGCTATTAACCGAGCGCTGCAATGCAATGAGACCTTACTAG 1749
DB 1312292 TTATGATTAACCCCAAAACCCAGCTCAAGCACTGTAAACATTTGAAACATTTGTTAG 1312233
CY 1750 TTCAATAGATCTTATGAAAGTCT-----CAGGCTTGCAGCATAT 1791
DB 1312232 TTCAATCTTCTATTTGTGAAGATTTTAACTTAAGTGTCTCTGACCTTTTCCGTAATA 1312173
CY 1792 TAGTAGCACTAAAAACAGAGAGTTAATTTATGTGAGACTTATTTGCGCAAAAGCTC 1851
DB 1312172 AGTAAATATATCATGCAAAATCCAGCACTTAATATTTGAAACAAAGCGGTTGCAATG 1312113
CY 1852 TGGATTTCCAAAAGCTTTTATTTCAATCAAGATTAATGTTCTATGCGCTGCACTGTTG 1911

Db 1312112 TCTGGCAATGACAGAAAAAGATTGCGAAAAAGATTGGGATCATTGATTTGAATGCG 1312053
 QY 1912 AGTTTGTGATGATGTTCAATGACCAATTTGACCATATTCATGTTATGAAAGTCTCATY 1971
 Db 1312052 TTGTTGTGAAAGATTTATGATCCGCTATGACATATCCGCAATATGTTACGCAACAT 1311993
 QY 1972 CAGATTGTATGCTCACTACAGATGATAGAGTGGAGAGACTTTCTAGCGAGTTGATA 2031
 Db 1311992 CTGAAAGTATTTAACTTCTTCCACAAAGCTTAGCCCGTCAATTTATCAATCAAGTTGATG 1311933
 QY 2032 GTGCTGCTGATTTCAATATGACAGATTCATCTGATGGGCTCGTTTGGATTGG 2091
 Db 1311932 CGGACCCGTTTATGTAATGACAGACACGCTTTATGATGCGGACATTTGATTTAG 1311873
 QY 2092 GTGCTGAGTTGGCATTAAGACAGGCGCTATCCATGCTGAGACCAAGTGGTGTGAAG 2151
 Db 1311872 GCGCAAGATTTGCGGAGATGACCAAAAATTGACGCTGTGGCCCAATGGGATTAGAAG 1311813
 QY 2152 GTCTTAATCAACAGATGATCTTGCAGG 2182
 Db 1311812 CATTAACCACTTAAATGGCTTTGTAAGG 1311782

RESULT 10

US-09-643-990A-1/c
 ; Sequence 1, Application US/09643990A
 ; Patent No. 6528289

GENERAL INFORMATION:

APPLICANT: Robert D. Fleischmann
 Mark D. Adams
 Owen White
 Hamilton O. Smith

TITLE OF INVENTION: The Nucleotide sequence of
 the Haemophilus influenzae Rd Genome, Fragments
 Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville,

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS V6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-Aug-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB186P1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-610-5790

TELEFAX: 310-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOROLGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Query Match 4.9%; Score 125.8; DB 4; Length 1830121;
 Best Local Similarity 45.9%; Pred. No. 1.2e-24;
 Matches 537; Conservative 0; Mismatches 607; Indels 27; Gaps 2;

QY 1039 CAGAGAACGAAAAAGATTTGCTAGATTTGGCAGATCTTTGGAGCAAAATGAGATTT 1098
 Db 1312952 CTGCTGAAAAAATTTGGAGATTTCATTTATTCAGAACATCGAACAAAGCAGCCG 1312893
 QY 1099 TAAATAGCTGTGAGATGAAAGCTGATGAGCTGCGGCCCAAGTGTGTGATATGAAAGC 1158
 Db 1312892 TTATCTTACGCGAAAAAGCAAAAGATTTGAACCTTCCAAAACAAAATGATATCGAGT 1312833
 QY 1159 CTTTGGTTGCTAGATTGACTATTAACAGAAAGATAGCAAGCTTTGCAAAATCTATTTC 1218
 Db 1312832 CTTGATGATTCCTTACTACTGCTACACAGAAAGCTTTACAGGCATTTGATATGATGAC 1312773
 QY 1219 GTACCTTGCAAAATATGAAAGACCTTATTAACCAATCTTAATAAAGACAGAGTTGCTG 1278
 Db 1312772 GCCACGTTATTTCTTAGACAGATCCGCTGGGAAAAATCATAGACGGCGGTACATGAGATA 1312713
 QY 1279 ATGATTTAGTTCTTGAAGAAACATCTTGCCCATTAAGTGTCTTAAATTTGTTTGAAT 1338
 Db 1312712 GCGGACTTAATATCGAACGCTGACGACTCGCTAGCGCTCATTTGTTATGAGT 1312653
 QY 1339 CCCGACCTGATGCTTGTGTTTCAATTTGATTCATCTTTGCAATTTGCAAGTGTATGTTCTTC 1398
 Db 1312652 CTGCGCAATATGTAACCATTTGATGAGTGGCAAGTCTTTGCCCTTAACCGGGTAAATGACATGA 1312593
 QY 1399 TCCATAAAGTGGAAAAAGAAAGCTATGACATCAACAGATATGCAATGCAATGATTAATGATG 1458
 Db 1312592 TTTTACCGGGTGTAAAGAAACACAGTTTCTTACAAAGTTTAAATGCAAGTTGTGCAAA 1312533
 QY 1459 ATGCTATTCCTGTAATGTTGTGAAAAACTTAATGCCC-----TTGTTACAATA 1509
 Db 1312532 ATGCTTTAGACAAAGCAGGCTTACCAAAATTTGCGGTCAGGCATTAACGATCCAAAC 1312473
 QY 1510 GAGATGATGACGAGATTTGCTAAAGCTTATGATGATGATGATGATGATGATGATGATGATG 1569
 Db 1312472 GTGAACCTGTTATGCAATTTTAAACTGATGCTATGAGATGATGATGATGATGATGATG 1312413
 QY 1570 GAAATTAAGCTTGTCTCTCAATCAAGGCTTCACTAAGATTCCTGTTCTTGGGATG 1629
 Db 1312412 GTGGTTGGGTTTACATGAAATTTGTAACAAATTCGATGATGATGATGATGATGATG 1312353
 QY 1630 CTGATGATATGCGACGTAATTTATGCAAAATGCTGACATGATGATGATGATGATGATGATG 1689
 Db 1312352 GTGCGGGTGTGTCATATCTTGTGAAAAAGTGGGATCAAAATTAAGCATTTTGTG 1312293
 QY 1690 TTGTAATGATGCAAAAGCTGATTACCCAGCAGCTGCAATGATGATGATGATGATGATGATGATG 1749
 Db 1312292 TTATGTAATACGCCAAGCAACCAAGCTGCAAGCCTGTAAACATTTGGAACATTTGTAG 1312233
 QY 1750 TTCAATAGATCTTATGAAAGATC-----CAGGCTTGAAGCACTAT 1791
 Db 1312232 TTCAACATTTCTATGCTGAAAGATTTTAACTTAACTTGTCTGACCTTTCCGCTAAA 1312173
 QY 1792 TAGTAGACCTAAAAAGAGAGATTAATTTATGTTGATGACCTATTGCCACAAAGCTC 1851
 Db 1312172 ACGTAAATATACGCAAAATCCAGCCTTAATATGTAAGAAACAGCGGGTGGCATG 1312113
 QY 1852 TGGGATTTCCAAAGCTGTTTCAATTTCAATCATGATGATGATGATGATGATGATGATGATG 1911
 Db 1312112 TCTGCAAGTACAGAAAAAGATTTGGAAAAAGATGGGATGTCATTTGATTTGATG 1312053
 QY 1912 AGTTTGTGATGATGTTCAATGACCAATTTGACCATATTCATGTTATGAAAGTCTCATY 1971
 Db 1312052 TTGTTGTGAAAGATTTATGATCCGCTATGACATATCCGCAATATGTTACGCAACAT 1311993
 QY 1972 CAGATTGTATGCTCACTACAGATGATAGAGTGGAGAGACTTTCTAGCGAGTTGATA 2031
 Db 1311992 CTGAAAGTATTTAACTTCTTCCACAAAGCTTAGCCCGTCAATTTATCAATCAAGTTGATG 1311933

QY 1631 TGATGTATATGCGACGTATATATGACAAATCAGCTGACATGATATGGCAAACTTAT 1690
DB 6499 GACTGGATGTTCCATGCTATGTGATGATGATGATGATGATGATGATGATGATGAT 6558
QY 1691 TGTAAATGATGCAAAATGATTTACCCAGACCTGCAATGCAATGAGACCTTACTAGT 1750
DB 6559 CATCAACATGCTAATAACAGTCGTCCTTCTGTTGTATGCAATGAGAGTTCTGCTGCT 6618
QY 1751 TCAT-----AGCATCTTATGAAAGTCAGGCTTGAAGCATATTTAGTACCTTAA 1804
DB 6619 TCATGAAAACAAAGGAGCAAGGCTTCTCTGCTGAGCAAGGTTGTTGAGAGCG 6678
QY 1805 AACAGAGAGAG-----TTAAATTTATGATGACCTTATGCGCAAAAGCTCT 1852
DB 6679 TAAGAGAGCTGACGTGCAACCAATTCATTCGCTATGATGCAAGAGCAAGCTTGT 6738
QY 1853 GGGATTTCCAAAGCTGTTTC-----ATTTCATCATGATGATGATGATGATGATGATGAT 1906
DB 6739 TTCAGGTCAAGAGCTGAGACCCAAAGACTTTCACACGAGTTTTCAGTATGCTTTC 6798
QY 1907 TGTGAGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1966
DB 6799 TGTGAGTTTGTGAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6858
QY 1967 TCATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2026
DB 6859 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6918
QY 2027 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2086
DB 6919 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6978
QY 2087 ATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2146
DB 6979 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7038
QY 2147 TGAG 2151
DB 7039 GAAAG 7043

RESULT 13
US-09-724-623-44
; Sequence 44, Application US/09724623
; Patent No. 6476209
; GENERAL INFORMATION:
; APPLICANT: Glenn, Mathew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 104801
; CURRENT APPLICATION NUMBER: US/09/724,623
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-09-724-623-44

Query Match 3.1%; Score 80; DB 4; Length 1254;
Best Local Similarity 44.5%; Pred. No. 3.4e-13;
Matches 470; Conservative 0; Mismatches 565; Indels 21; Gaps 3;

QY 1167 GCTAGATGATCTTAAACAGAGAAAGATGACAGCTTGCAGAAATCTTTCGTAACCTT 1226
DB 202 GATCGATTTGTTACTGACAGCGCGGATTTGCTGATGATGATGATGATGATGATGATGAT 261
QY 1227 GCAATATGAGAGACCTTAAACAGATGATCTTAAACAGAGAGGTTGCTGATGATTTA 1286
DB 262 GCGGCTTACTGATCTCAACCGCCGACAGGATTAAGGCTGGGTGATGATGATGATGATGATG 321

QY 1287 GTTCTTGAGAAAACATCTTCCCATTTAGGTGTTCTTATTTGTTTGAATCCGACCT 1346
DB 322 AATATGCGCAAAAGAGGATCTTTAGGAGTGGTGGATATTTATGAGCGCGGCA 381
QY 1347 GATCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1406
DB 382 AATGTAACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 441
QY 1407 GGTGAAAAGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1466
DB 442 GCGGTAAGAGCGCTGACAGCAATTTGCGTGGACACCGTTTACAGGCTGATG 501
QY 1467 CCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1517
DB 502 ACCGACAGAGATGTCGAAAAGAGCGATTCATTTATACGAGACCGGAGAGAGAGT 561
QY 1518 ATGCAAGATTTGCTAAAGCTTATGATGATGATGATGATGATGATGATGATGATGAT 1577
DB 562 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 621
QY 1578 AAGCTTGTCTCAATCAAGAGCTCAATTAAGATTCCTGTTCTTGGGATGATGAT 1637
DB 622 GGTGATTAAGAGATGCTTGAACGCTTACCGTACCGTATTTGAAACCGGCGGCG 681
QY 1638 ATATGCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1697
DB 682 AATGTCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741
QY 1698 GATGCAAAATGATTAACCAAGAGCTCAATTAAGATTCCTGTTCTTGGGATGATGAT 1757
DB 742 AACGCAAGTATGAGCGCGCTGTTGTAAGAGCGCGGCAAACTTTATTAATCAAGCT 801
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DB 1219 TATCAGGTGCTGATTAACGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1254

RESULT 14
US-09-107-532A-2515
; Sequence 2515, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

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1      NUMBER OF SEQUENCES: 7310
2      ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
3      CORRESPONDENCE ADDRESS:
4      ADDRESSEE: GENOME THERAPEUTICS CORPORATION
5      STREET: 100 Beaver Street
6      CITY: Waltham
7      STATE: Massachusetts
8      COUNTRY: USA
9      ZIP: 02354
10     COMPUTER READABLE FORM:
11     MEDIUM TYPE: CD-ROM ISO9660
12     COMPUTER: PC
13     OPERATING SYSTEM: <Unknown>
14     SOFTWARE: ASCII
15     CURRENT APPLICATION DATA:
16     APPLICATION NUMBER: US/09/107,532A
17     FILING DATE: 30-Jun-1998
18     PRIOR APPLICATION DATA:
19     APPLICATION NUMBER: 60/085,598
20     FILING DATE: 14 May 1998
21     APPLICATION NUMBER: 60/051571
22     FILING DATE: July 2, 1997
23     ATTORNEY/AGENT INFORMATION:
24     NAME: Atinello, Pamela Deneke
25     REGISTRATION NUMBER: 40,489
26     REFERENCE/DOCKET NUMBER: GTC-012
27     TELECOMMUNICATION INFORMATION:
28     TELEPHONE: (781) 893-5007
29     TELEFAX: (781) 893-8277
30     INFORMATION FOR SEQ ID NO: 2515:
31     SEQUENCE CHARACTERISTICS:
32     LENGTH: 462 base pairs
33     TYPE: nucleic acid
34     STRANDEDNESS: double
35     TOPOLOGY: circular
36     MOLECULE TYPE: DNA (genomic)
37     HYPOTHETICAL: NO
38     ANTI-SENSE: NO
39     ORIGINAL SOURCE:
40     ORGANISM: Enterococcus faecium
41     FEATURE:
42     NAME/KEY: misc feature
43     LOCATION: (B) LOCATION 1..462
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45     US-09-107-532A-2515
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47     Query Match          2.9%; Score 74.6; DB 4; Length 462;
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49     Matches 155; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
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51     QY      1906 CTGTTGAAGTTGTTATGATGATGTTCAATCAGCAATTTGACCATATTCATGTTATGGAAGTG 1965
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71           |||||

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Sequence 2 Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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Query March 2.9%: Score 72.8; DB 3; Length 4403765;
Best Local Similarity 52.3%; Pred. No. 9.6e-09;
Matches 161; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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QY 1944 CATTTTCATCGTATGGAAGTGTCTCATAAGATTTGATTCGTCATCAGATGATTAAGSTA 2003
Db 2721305 CATATCAACAATACGCGACCGGGACACAGAAAGCATGTGACACCAATCTTGATGCG 2721246

QY 2004 GCAAGACCTTTCTACGCAAGTGTGATAGTGTCTGTATTTCAATAATGCAAGTACAGA 2063
Db 2721245 GCCCAAGCTTTACGAAACAGATGATGCGCGCGGTGATGTTGAACGATCAACGGCG 2721186

QY 2064 TTCTCTGATGCGGCTGCTTTTGGATTTGGGTGTGAGTTTGGCATTAACACAGGCGGTATC 2123
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Search completed: March 10, 2004, 12:06:50
Job time : 200.536 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2004, 10:31:30 ; Search time 9652.81 Seconds

(without alignments)
11544.306 Million cell updates/sec

Title: US-10-026-767-2

Perfect score: 2571

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank:*

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2: gb_hcg:*

3: gb_in:*

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23: em_pat:*

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27: em_seg:*

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29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

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40: em_hcgo_mus:*

41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2569.4	99.9	2600	8	AY080771
3	2561.4	99.6	2571	8	ATPATPSCS
4	2559.8	99.6	2584	8	ATPSCOSMR
5	2537	98.7	2552	8	ATPSCSAGN
6	2185	85.0	2185	8	AY150430
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8	2154	83.8	2154	6	AY113046
9	1864.6	72.5	2551	8	AF314811
10	1673.4	65.1	2440	8	ATPSCS2
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12	1669.8	64.9	2181	6	AX507171
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ALIGNMENTS

RESULT 1

AF424633

LOCUS

DEFINITION Arabidopsis thaliana At2g39800/T517.10 mRNA, complete cds.

ACCESSION AF424633

VERSION AF424633.1 GI:15983516

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidops.

REFERENCE

1 (bases 1 to 2630)

Shim, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Bohn, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D.,

QY	1081	CGATGCCCTTGAAGCAAAATGTTATCTACATCAAAAGCTGAGATAGTATGATGCTTC	1144
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Db	1874	GAACTATCACAAAGAGAGCGTCACTTAAACAGTAGATCTGTGCGCAAGGCTTGCATCTTTGA	1933
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QY	2461	ACCACTTAGTCTTGTCTCATAGTACGATGGAAGAACATTTAATTAGCTTCTCTTGTGCA	2520
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RESULT 2
AY080771

LOCUS AY080771 2600 bp mRNA linear PLN 18-SEP-2002
DEFINITION Arabidopsis thaliana putative delta-1-pyrrolone 5-carboxylase
synthetase P5C1 (At2g39800) mRNA, complete cds.

SOURCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons: core eudicots: rosids, eurosids II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORS

Goulden, L.A.D., Lee, J.W., Quach, H.N., Talamantes, A.C., P. Carinici, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kariya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Saeou, M., Seki, M., Shim, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

REFERENCE

Deng J.M., Goldsmith A.D., Jee J.M., Onodera C.S., Quach H.L., Tang C.C., Toriomi M., Wu H.C., Yamamura Y., Yu G., Bowser L.L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ichida J., Jones T., Kaniya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Mirada M., Natsusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Eckert J.R. and Theologis A.

JOURNAL

COMMENT

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RATL cDNAs: Yamada, K., Bahr, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. V., Deng, J. M., Hayashizaki, Y. and Shinozaki, K.

Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Tortum, M., Wu, H.C., Yamamura, Y., Yu, G., Bower, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kam, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shin, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

FEATURES

SOURCE

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gene

5' UTR

CDS

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ORIGIN

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Matches 2570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 421 TTACTATGAGCTATGTTTATGACAGCTTGATGATGAGGAGGCTCACTTGTGAGAAATGA 480
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RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source	gene	CDS
RESULT 3	ATATP5CS	ATATP5CS	2571 bp	RNA	linear	PLN 07-FEB-1999	Arabidopsis thaliana	Arabidopsis thaliana mRNA for delta1-pyrroline-5-carboxylate synthase, complete cds.														
LOCUS	ATATP5CS	2571 bp	RNA	linear	PLN 07-FEB-1999																	
DEFINITION	ATATP5CS	2571 bp	RNA	linear	PLN 07-FEB-1999																	
ACCESSION	D32138	GI:1532270																				
VERSION	D32138.1	GI:1532270																				
KEYWORDS	ATP5CS; delta1-pyrroline-5-carboxylate synthetase.																					
SOURCE	Arabidopsis thaliana	(thale cress)																				
ORGANISM	Arabidopsis thaliana																					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside II; Brassicaceae; Arabidopsis.																					
AUTHORS	1 (bases 1 to 2571)																					
TITLE	Yoshida,Y., Kiyosue,T., Katagiri,T., Ueda,H., Misoeguchi,T., Yamaguchi-Shinozaki,K., Wada,K., Harada,Y. and Shinozaki,K.																					
JOURNAL	Correlation between the induction of a gene for delta																					
MEDLINE	1-pyrroline-5-carboxylate synthetase and the accumulation of																					
PUBMED	proline in Arabidopsis thaliana under osmotic stress																					
REFERENCE	Plant J. 7 (5), 751-760 (1995)																					
AUTHORS	Yoshida,Y.																					
TITLE	2 (bases 1 to 2571)																					
JOURNAL	Submitted (12-JUL-1994) Yoshu Yoshida, Hitachi Ltd., Advanced																					
MEDLINE	Research laboratory, Hatoiyama, Hiki-gun, Saitama 350-03, Japan																					
PUBMED	(Tel:0492-96-6111, Fax:0492-96-6006)																					
REFERENCE	On Sep 12, 1996 this sequence version replaced gi:938020.																					
AUTHORS	Location/Qualifiers																					
TITLE	1..2571																					
JOURNAL	/organism="Arabidopsis thaliana"																					

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2571
/gene="ATP5CS"

Query Match 99.6%; Score 2561.4; DB 8; Length 2571;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2565; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ORIGIN

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1 CCGATTTTATTTTCTTACCTTAATAACGACGCTCTTCACTAGATCCGACTCACTTAAAC 60
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RESULT 5
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 ACCESSION X86777
 VERSION X86777.1 GI:870865
 KEYWORDS p5csA gene; pyruvate-5-carboxylate synthetase A.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Strizhov,N., Abraham,E., Okresz,L., Bliokling,S., Zilberstein,A.,

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DEFINITION Arabidopsis thaliana delta-1-pyrroline 5-carboxylase synthetase
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ACCESSION AY150430
 VERSION AY150430.1 GI:23297450

KEYWORDS Eukaryotes; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 ORIGIN Arabidopsis thaliana (thale cress)
 SOURCE FRI CDNA

REFERENCE 1 (bases 1 to 2185)
 Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Quach, H.L., Tang, C.C., Tortum, M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
 Arabidopsis Open Reading Frame (ORF) Clones

TITLE JOURNAL
 REFERENCES
 AUTHORS
 Unpublished
 2 (bases 1 to 2185)
 Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Quach, H.L., Tang, C.C., Tortum, M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
 Arabidopsis Open Reading Frame (ORF) Clones

TITLE JOURNAL
 COMMENT Submitted (13-SEP-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
 Annotation is based on the January 2002 version of the Arabidopsis genome submitted to Genbank.

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ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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REFERENCE
1 Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 1391 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations AG
(CH)

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 rosids; eustroids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE
 1 (bases 1 to 2551)
 Kang, Y. H. and Lee, S. Y.
 TITLE Isolation of a gene encoding the delta 1-pyrroline-5-carboxylate
 synthetase A in Brassica napus
 JOURNAL Unpublished
 REFERENCE
 2 (bases 1 to 2551)
 Kang, Y. H. and Lee, S. Y.
 AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (19-OCT-2000) Lab. of Biochemistry, Graduate School of
 Biotechnology, 1, 5-Ka, Anam-dong, Sungbuk-ku, Seoul 136-701,

Rep. of Korea
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 1 (bases 1 to 2440)
 Strizhov,N., Abraham,E., Okresz,L., Bickling,S., Zilberstein,A.,
 Schell,J., Koncz,C. and Szabados,L.
 Differential expression of two P5CS genes controlling proline
 accumulation during salt-stress requires ABA and is regulated by
 ABI1, ABI1 and AXR2 in Arabidopsis
 Plant J. 12 (3), 557-569 (1997)

MEDLINE 98012527
 PUBMED 9351242
 REFERENCE 2 (bases 1 to 2440)
 AUTHORS Strizhov,N.
 TITLE Direct Submission
 JOURNAL Submitted (11-NOV-1996) N. Strizhov, Max-Planck-Inst. fuer
 Zuechtungsforsh., Abt. J.Schell, Carl-Von-Linne-Weg 10, D-50829
 Koeln, FRG
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 1 (bases 1 to 2517)
 Shim, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Ban, J.,
 Bower, L., Carninci, P., Chang, B., Dale, J.W., Goldsmith, A.D.,
 Hayashizaki, Y., Ishida, J., Jones, T., Kamitani, A., Karlin-Neumann, G.,
 Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,
 Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
 Satou, M., Seki, M., Southwick, A., Tang, C.C., Tortolani, M., Wu, H.C.,
 Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
 Theologis, A. and Ecker, J.R.
 Arabidopsis cDNA clones
 Unpublished
 2 (bases 1 to 2517)
 Shim, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Ban, J.,
 Bower, L., Carninci, P., Chang, B., Dale, J.W., Goldsmith, A.D.,
 Hayashizaki, Y., Ishida, J., Jones, T., Kamitani, A., Karlin-Neumann, G.,
 Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,
 Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
 Satou, M., Seki, M., Southwick, A., Tang, C.C., Tortolani, M., Wu, H.C.,
 Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
 Theologis, A. and Ecker, J.R.

TITLE

Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinzaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

JOURNAL

Direct Submission

Submitted (26-MAR-2002) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Shim, P., Chen, H., Cheuk, R., Kim, C.J., Meyer, M.C., Bahi, J., Bowser, L., Chang, B., Dale, J.M., Goldsmith, A.D., Jones, T., Katlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Shim, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinzaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match 65.1%; Score 1673.4; DB 8; Length 2517;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 1854; Conservative 0; Mismatches 301; Indels 0; Gaps 0;

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455 GGTGCTCAAGTCTGAGTATGAGCAAGTATGAGCAAGTATGAGCAAGTATGAGCAAGTATGAGCA 514
517 TAATGAAGCTGCAAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 576
515 TAGTGAAGCTGCAAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 574
577 TGTATATGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 636
575 TGTATATGAGCAAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 634
637 TAGCTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 696
635 CAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 694
697 TGTGAGGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 756
695 TGTGAGGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 754
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755 CATTGAAGGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 814
817 GGTGATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 876
815 GGTGATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 874
877 CATTGAAGGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 936
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937 AACCTGTTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 996
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995 CATTGAAGGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 1054
1057 GAAAGGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 1116
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1177 TCGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 1236
1175 TCGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCTTATGAGCT 1234
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1295 TTATGAGGATTCATCGGCGTGTGTTTAAAGAAACAGAGTGGCAGATGCTTGT 1354
1357 TGAATGAGGATTCATCGGCGTGTGTTTAAAGAAACAGAGTGGCAGATGCTTGT 1416
1355 TGAATGAGGATTCATCGGCGTGTGTTTAAAGAAACAGAGTGGCAGATGCTTGT 1414

Db	841	CATCAAGATGCTCATTTATATGAGGCTCCGGTGTGATATCTACTTCTCGGACATGGCAGTT	900
Qy	1007	GCTGCGAGGGAAGAGTTCCAGAAAGCTTCAGGCTTTATCTTGGAAAGCAGAGAAAAATT	1066
Db	901	GCTCCAAAGGGGAAGAGCTCAAGAAAGCTTCAGGCTTATCTTCAGAAAGATAGAAACAAATT	960
Qy	1067	CTGCTTATATATTCGGCAGTCCCTTGAAGCAAAATTATCTCAATCAAGAGCTGAGATATG	1126
Db	961	CTACACGACATATGCCATATGCCCTTGAAAGTAAATAGAAAACAATTAAGCTGAGATATGAT	1020
Qy	1127	TTAATATGATCTTCTGCACAAAGAGCTGGGTTGGAAGATCAATATGTTGGCTCGTTAGTT	1186
Db	1021	TTAATATGTTGGTCGAGCACAAGAGAGCTGGAATATGAAGTCTTTGGTATGCTCGCTTAGTT	1080
Qy	1187	ATGACACCTGAAAGATCTCGAGGCTTGACACTCAGTTGGTAACTAGAGTATATGAA	1246
Db	1081	ATGAAGCTTGGAAAGATTCAGAGCTTTGACACTTCGTTCCGCACTAGCCGAATGAA	1140
Qy	1247	GATCCAAATCGGCGGTGTTTTAAAGAAAACAAGGTGGCAGATGGTCTGTCTTAGAAG	1306
Db	1141	GATCCAAATAGAGCCGGTATTTAAAGAAAACTCAGGTGGACATATCTTATTTTAGAAG	1200
Qy	1307	ACCTCATACCATTAAGGGTACTTCTGATTTTGTAAATCCGACCTGATAGCATTTGTA	1366
Db	1201	ACCTCATACCAATATAGGTGTCTTCTGATTTTGTAAATCCGACCTGATAGCATTTGTT	1260
Qy	1367	CAGATATGCTTCACTTGCACATCCGTAAGTGAATAGTCTTCTGCTGAAGGGGTGAAGAG	1426
Db	1261	CAGATATCTTGCCTTGCAATCCGAGTGAATATGTCTTCTGCTGAAGGGGTGAAGAGAG	1320
Qy	1427	GCCCGGCGCATCAATATGCTATCTTACACAAGTGATCACTGATGCAATTCAGAGACTGT	1486
Db	1321	GCTGTCATCAATAATGCTATCTTACACAAGGTGATCACTGATGCAATTCGGAACGTGT	1380
Qy	1487	GAGGGTAAACCATATGACCTTGCTGCTTCCAGAGAGAGATTCCTGATTTGCTTAAGCTT	1546
Db	1381	GAGGTAAACCATATGACCTTGCTGCTTCCAGAGAGAGATTCCTGATTTGCTCAAGCTT	1440
Qy	1547	GATGACGTTATCGATCTTGTGATGCCAAGAGAAACAACAAGCTTGTACTCAGATAAA	1606
Db	1441	GATGACGTTATGTTAGTCTTGTGATCCCAAGAGAGCAACAAGCTTGTCTCAATAAAA	1500
Qy	1607	AAATCTACAAAATATCCCTGCTGATAGTCAATGCTGATGGAATCTGTCAATATATAGTGAC	1666
Db	1501	AATCTGACAAAATATCCAGTGTATGAGCCATGCTGATGGAATCTGTCAATATATATGTGAT	1560
Qy	1667	AAGCTTGTGATACGGAATATGGCAAGCGCATAGTTTGTGATGCAAAATTTGGAATATCCA	1726
Db	1561	AAGTGTGTTAAACGTGACATGGCAAGCGCATAGTTTGTGATGCAAAATTTGGAATATCCA	1620
Qy	1727	GCAAGCTGTATATGCGATGGAACCTTCTTGTGATTAAGATCTTAGACAGAAATGCTGTG	1786
Db	1621	GCAAGCTGTATATGCGATGGAACCTTCTTGTGATTAAGATTTTGGACACAATATGTTTT	1680
Qy	1787	CTTAATAGCTTATTTTGTCTGTGACAGCAATGAGTCACTTTGTATGTGACCAAG	1846
Db	1681	CTGATGATCTTATTTATTTATGTTCTGAAACCAAGGCGTCACTTTGTATGTGTGGCCAAAG	1740
Qy	1847	GCAAGTAAAGATATCTGAACATACAGAAAGCAGGTCAATTCACATAGTACTGTGCCAAG	1906
Db	1741	GCAAGTAAAGATATCTGAACATATTCGGAACAATAATCATTTTCAACAGATACAGTTCCAAG	1800
Qy	1907	GCTTGCACTGTGAATGTATGTAAGAACGTTTATGTGTATATAGATCAATTCACGCAAT	1966
Db	1801	GCTTGCACTGTGAATGTATGTAAGAACGTTTATGTGTATATAGATCAATTCACCAAT	1860
Qy	1967	GGAAGTGCACACACAGACTGCAATTTGTGACAGAGATCAAGATTTGACAGACTATTCCTT	2026
Db	1861	GGAAGTGCACACACAGATTTGCAATTTGTGACGGAAGATAGGAAGTGTGACGAATATTCCTC	1920
Qy	2027	CGCCAGATGGAATAGGCTGTCTGTCTTCCACAACGCGACACACAAGTTCTCGATGTGTT	2086
Db	1921	CGCCAGATGGAATAGGCTGTCTGTCTTCCACATGTGAACACACAAGTTCTCGATGTGTTT	1980

	RESULT 13	
	AFJ14812	
	LOCUS	Brassica napus delta 1-pyrroline-5-carboxylate synthetase B mRNA,
	DEFINITION	complete cds.
	ACCESSION	AFJ14812
	VERSION	AFJ14812.1 GI:12667250
	KEYWORDS	.
	SOURCE	Brassica napus (rape)
	ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosoid II; Brassicales; Brassicaceae; Brassica.
	REFERENCE	1 (bases 1 to 2529) Kang,Y.H. and Lee,S.Y. Isolation of a gene encoding the delta 1-pyrroline-5-carboxylate synthetase B in Brassica napus
	AUTHORS	Unpublished
	JOURNAL	2 (bases 1 to 2529) Kang,Y.H. and Lee,S.Y. Direct Submission Submitted (19-OCT-2000) Lab. of Biochemistry, Graduate School of Biotechnology, 1, 5-ka. Anam-dong, Sungbuk-ku, Seoul 136-701, Rep. of Korea
	JOURNAL	Location/Qualifiers
FEATURES	source	1..2529
		/organism="Brassica napus"
		/mol_type="mRNA"
		/db_xref="taxon:3708"
CDS		120..2303
		/note="BnpSc62"
		/codon_start=1
		/product="delta 1-pyrroline-5-carboxylate synthetase B"
		/db_xref="GI:12667251.1"
		/translation="MEDIDRSRAPADQVRIYVKGTAVVTGKGRLALGRIGATGE QALAINSDGFENVLLIVSGAVGLQRRLRYQLVNSSPADLQKPELTLDGACAGGOS SLNAVETPMDVDVVAQMLVTDSPRDQFRQQLSEYTKAMIKMVEFVENDDAI STRAPAKDSTGIFMNDISLAALLAILKIDLILSDVGLVGPSPDKSLIHTY VKHGKEITFGIEKSRRLRGGMATKAYAAVNAAGCPVITITSGLAENIAKLKGR VGTLEPHDDAHMARVVDTTTRDMAVARRESRKLIQALSDDRKNILLDIANALEANER KLRKENDVLAAROEAGEERSIVARIMYMGKLSISAASIROLAEEMDPICRVLYKTBE VADSLILEKTSRPSPTVILLIPESRPDLVYLASAIRSGNGLIKGGKAPRNAILH LKVDAIDLPKTVVGKLTGLVTSRBDIPFLKDDVIDLVTPRGSKLYSQIKNSKITPY LGHADGICHVYVKSICVMAKRVSDAKLDYPACAMETVLVHKDLBONGUNELILI VALQANGVTLVYGGPKAGKCLNIPEVKSFNHEYSKACTVIIVEGHGAIDHIHQGSBA HTDIOANGDEVSAEIIPLROYDSAIVINASTRFCDGRFGIGALEVGISSTRIHARGPVS GVEGLLTRWIMRGQGVVDGDNGVAVTHKDLPLYLERTKAVONQH"
ORIGIN		
	Query Match	64.7%; Score 1662.4; DB 8; Length 2529;
	Best Local Similarity	85.0%; Pred. No. 0;
	Matches 1668; Conservative	0; Mismatches 329; Indels 1; Gaps 1
Oy	CTCTCTCGTGATGGTTTGTGTAGACGACACAGCATATGAGAGAGCTTAGTCCTC	126
Dp	CTCTCTCTCTCTCTCTTTTGG-ATAAGAAGCTAGCTATGAGAGATGAGTAAGATCGTTC	142
Oy	127 ACGTGCCTTTGCCAGAGACGTCACAAAGTATCTGTTAAAGTTGGAGACAGCACTTTTAC	186

143 CCGGCGCTTTCGCAAGAGAGCTTAAGCGTATCGTTGCAAGGTTGGGACAGAGTTGTAC 202
187 TGAAGAAAGTGAAGAGTGGCTCTTGCTTTAGAGACACTGTGTGAACAGTTGGCGA 246
203 AGGAAAGGTGAAGAGTGGCTCTTGCTTTAGAGAGCTATCTGGAGACAGTTGGCTTA 262
247 ATTAACTCGAGTGAATTTAGAGTGAATTTGTGTCACTGTGTGGGTTGTCTTGGCAG 306
263 ATTGAATCGGAGTGGTTTGAAGTCAATTTGTGTCTGTGTGGGTTGTCTTGGTGT 322
307 GCAGAGCTTCGTTATCGACATTTAGTCAATAGCAGCTTTGGGATCTTCAAGAGCTCA 366
323 TCAGAGGCTTGAATACAGACATTTAGTCAACAGAGCTTTGACAGCTTCAAGAGCACA 382
367 GACTGAATCTGATGGAGAGGCTTGTGTGTGTGTGACAAAGAGAGCTTATGCTTACTA 426
383 GACTGAATCTGATGGAGAGGCTTGTGTGTGTGTGACAGAGAGCTTCAAGCTTACTA 442
427 TGAAGCTATGTTGACCAAGCTTGTATGACGAGCTCAACTTGTGTATGACAGTAG 486
443 TGAAGCTATGTTGACCAAGCTTGTATGACGAGCTCAACTTGTGTATGACAGTAG 502
487 TTTTGAAGACAAAGATTTTCAGAGACACTTATGAACTGTCAAGTCTATGCTTGAATT 546
503 TTTTGAAGATGAAGATTTTCAGAGACACTTATGAGACAGTCAAGCTATGCTTGAATT 562
547 GAGGATATTCATTTTCATGAGATGATGCTATTTAGACACCCGAGAGCCCATATCA 606
563 GAGAGTTATTCAGTTTTCAGAGAGATGATGCTATTTAGACCTCGAAAGCCCTTTTACA 622
607 GGAATCTCTGTATTTTTCGAGATACAGATAGCTTATGCTTCACTGAGCTTGAAT 666
623 GGAATCTCTGTATTTTTCGAGATACAGATAGCTTATGCTTCACTGAGCTTGAAT 682
667 GAAAGCTATCTCTATCTCTGTAGCGATGTTGAGAGCTTTCACAGAGCCCTCCAG 726
683 GAAAGCTATCTCTATCTCTGTAGCGATGTTGAGAGCTTTCACAGAGCCCTCCAG 742
727 TGAATCTATCTCAAGATTTTCACACTTTTGTAAAGAAAACATCAAGATGATTTAC 786
743 CGATCTTAAAGTCAAGATTTTCACACTTTTGTAAAGAAAACATCAAGATGATTTAC 802
787 ATTGCGCGCAATTCAGATTTAGAGAGAGGAGTATGATCTGAAAGTCAAGCTGAGT 846
803 CTTTGCAGAGATTCAGATTTAGAGAGAGTATGATCTGAAAGTCAAGCTGAGT 862
847 CAATGAGCTTATGCTGGAGTCTGTCTCATCAATACAGAGGATTTTCAAGTGAAGAT 906
863 TATGAGCTTATGCTGGAGTCTGTCTCATCAATACAGAGGATTTTCAAGTGAAGAT 922
907 AGATTAAGTCTTCAAGAGCTATGCTGTGAACCTTGTTCATCAAGATGCTGTTTATG 966
923 AGCTTAAGTCTTCAAGAGCTATGCTGTGAACCTTGTTCATCAAGATGCTGTTTATG 982
967 GGTCTGATCAAGATTTCAATGCTGTGTGATGAGAGTGTGTGAGAGGAAAGTTTCAAG 1026
983 GGTCTGATGCTGATCAATGCTGTGTGATGAGAGTGTGTGAGAGGAAAGTTTCAAG 1042
1027 AAAGCTTCAAGGCTTATCTTGTGAGAGACAGAAAAAATTTGCTGTGATTTCCAGATG 1086
1043 AAAGCTTCAAGGCTTATCTTGTGAGAGAGAAAAAATTTGCTGTGATTTCCAGATG 1102
1087 CCTTGAAGCAAGATTTATCAATCAAGCTGAGATGATTTGATTTAGCTTCTGACACA 1146
1103 TCTTGAAGCAAGATTTATCAATCAAGCTGAGATGATTTGATTTAGCTTCTGACACA 1162
1147 AGAGGCTGAGTGAAGAGTCAATGCTGCTGCTTATGATGACCTGAGAAAGATCTC 1206
1163 AGAGGCTGAGTGAAGAGTCTTGTGATGCTTATGATTTAGAGGCTGAGAAAGATCTC 1222
1207 GAGCTTGAAGCTTCAAGTGTGATGCTTATGAGAGATCAAGTGGGCTGTTT 1266

1223 AAGCTTGCAGCTTCTATGCGCAGCTAGCTGAATGGAAGAACCAATGGTGTGTTCT 1282
1267 AAAGAAAACAGAGTGGAGATGCTTTGCTTTGAGAAAGACTCATACCATTTAGCGT 1326
1283 AAAGAAAACAGAGTGGAGATGCTTTGCTTTGAGAAAGACTCATACCATTTAGCGT 1342
1327 ACTTGTGATTTTGTGATTTCCGACCTGATGACCTGTGTACAGATACCTTCACTTGGCAT 1386
1343 TCTTGTGATTTTGTGATTTCCGACCTGATGACCTGTGTGTACAGATACCTTCACTTGGCAT 1402
1387 CCGTATGAGAAATGCTTCTTGTGAGAGGAGTGAAGAGAGCCCGGATCAATGCTAT 1446
1403 CAGAGTGGAAATGCTTCTTGTGAGAGGAGTGAAGAGAGCCCGGATCAATGCTAT 1462
1447 CTTACAGAGGATGCTGATGCAATTCAGAGAGCTGTGGGGTGAATCAATGCTAT 1506
1463 CTTACAGAGGATGCTGATGCAATTCAGAGAGCTGTGGGGTGAATCAATGCTAT 1522
1507 TGTGATTCAGAGAGAGATTCCTGATTTGCTTAACTTATGACCTTATGATCTTGT 1566
1523 TGTGATTCAGAGAGATGATGATTCCTGATTTGCTTAACTTATGATGATGATCTTGT 1582
1567 GATCCAGAGAGAGAGAGAGAGCTTGTCTCAGATTAATAATAATCTTGT 1626
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1627 GCTAGTCTATGCTGATGAAATCTGATGATTAATGTCAGAGAGCTTGTATGAGAT 1686
1643 GCTAGGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1702
1687 GCGAAG 1746
1703 GCGAAG 1762
1747 AACCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1806
1763 AACCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1822
1807 TCTGAG 1866
1823 CTTGAG 1882
1867 ACCGAG 1926
1883 TCCGAG 1942
1927 AG 1986
1943 AG 2002
1987 CATTGAG 2046
2003 CATTGAG 2062
2047 TGTGTTCAAG 2106
2063 TGTGTTCAAG 2122
2107 GGTGGGAG 2166
2123 GGTGGAG 2182
2167 TACAG 2226
2183 GACAG 2242
2227 TTAACAG 2264
2243 TTAACAG 2280

RESULT 14
ADU92286

LOCUS	ADU92286	2378 bp	mRNA	linear	PLN 22-APR-1998
DEFINITION	Actinidia deliciosa pyrrolidine-5-carboxylate synthetase mRNA,				
ACCESSION	U92286				
VERSION	U92286.1	GI:1928959			
KEYWORDS					
ORGANISM	Actinidia deliciosa				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Ericales; Actinidiaceae; Actinidia.				
REFERENCE	1 (bases 1 to 2378)				
AUTHORS	Walton,E.F., Podivinsky,E., Wu,R.-M., Reynolds,P.H.S. and Young,L.W.				
TITLE	Regulation of proline biosynthesis in kiwifruit buds with and without hydrogen cyanamide treatment				
JOURNAL	Physiol. Plantarum 102, 171-178 (1998)				
AUTHORS	Walton,E.F., Podivinsky,E., Wu,R.-M., Reynolds,P.H.S. and Young,L.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-MAR-1997) HortResearch, Private Bag 3123, Hamilton, New Zealand				
FEATURES					
source	Location/Qualifiers				
	1..2378				
	/organism="Actinidia deliciosa"				
	/mol_type="mRNA"				
	/db_xref="taxon:3627"				
	/cissue_type="axillary bud"				
	9..2162				
	/codon_start=1				
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	/protein_id="AA014481.1"				
	/db_xref="GI:1928960"				
	/translation="MDAVDSTRFAVKKVRLIKVAVYTRADRLALGLALCEQIHENLSSQFEVILVTSAGVGRQRLPYRKIVNSFPDLKPELELGKCAAVGQNGLIALYDPLFSQLDVTSQQLVLTVDNDFDPERKQLTEVSLNLKVIPIFENDAVSTRKPEVDASGIPMDNDSALALALEKADLVLTIVVEGVSSEPDPSKLIHNYIKEMEGELITGDKRVRGGWTAVKVKAIVAAHGIIVITGCAATNIIKVGUQGEI GLTPHRDAOKMAPVYGDCARDMVAABSSRRLOMSPPRSKILLDVADALANNEQLIRINENADLAAQAGVEKSLIRLAKSGISLASIVLANMEPCHIVLRTETIDGVLAKTSSPDLVLLIFESPDAVLQVLSLIRSGNGLVAKGGEARSNALIKVITSAIPENYVDPRLIGLVTSREI.PDLKLDDVDIVIPGSMNVSOIKESKIPVLGHADGIVHYVVDKSNANDMAKRVLLDKTQTPAPACAMEILLVHKDLVQNGCDELIV ELQIKGVAVIHGSPRASSLIIH PEARSSLNHEYSLACTIEIVDVYAAIDIIHHGSPV TDSITTEDHVAEIRFOVDSSSVLHNASIRFSGARFGIAGVIGISTRIIHARGPVGVEGLLTRWLRARSGGVDDDKGIYVTHKDLTSHA"				
ORIGIN					
Query Match	48.4%; Score 1243.8; DB 8; Length 2378;				
Best Local Similarity	73.5%; Pred. No. 2.3e-312;				
Matches 1587;	Conservative 0; Mismatches 572; Indels 0; Gaps 0;				
Dy	102 CGATAATGAGAGAACTAGATGCTTCAAGTGTTTGGCAGAGACGTCAAAAGTATGCTGC	161			
Db	4 CAACAATGAGACGAGTGCATTCAACGCGAGCTTCGTCAAAGCGCTGAAAGGTGTATCA	63			
Dy	162 TTAAAGTTGGACACGAGTGTCTTAATCTGAAAAAGGTGAAAGATTGGCTTGGTCTTAA	221			
Db	64 TCAAGTTGGGACCTGCTGTGTCTCACTCAGCTAGCTATGAAAGCTGGCACTTGAAGACTTG	123			
Dy	222 GAGACATGTGGAACAGCTTGGCGGAATTAACCTCCGATGATTTGAGTGATATTTGGTGT	281			
Db	124 GAGCATTTGTGAGCAATTCATGAATCTGAATTTCTCAAGAAATTTGAGGTATTTTGGTTA	183			
Dy	282 CATCTGATCGGTTGATCTTTGGCAGAGCAAAAGCTTCGTTATGCAATTTAGTCATATGCA	341			
Db	184 CATCAGGTGCTGTTGTGTGTGGCCGCAACGGTTAAGATCCGGAATTTGTCACACGCA	243			
Dy	342 GCTTTGGCAATCTTCAGAAAGCTCAGACTGAATCTGAATGGAAAGGCTTGTGCTGGTGG	401			
Db	244 GCTTGTGTAATCTTCAAAGACCAATTTAAATCTGAATGGAAAGGCAATGTGCAAGCTTGG	303			

QY	402	GACAAAGCAGTCTTAAGCTTAACATATGAGCTAATGTTGACACAGCTTGAATGACGGACG	461
Db	304	GGCAAAATGGTCTATTGGCTCTCTATGATCAATGTTTAACTAGTCAGATGATGACATCG	363
QY	462	CTCACTTTGGTGAATGACAGTAAGTTTAAAGACAAGATTTTCAGAGCAACTTAATG	521
Db	364	CTGAGTACTCGTTTCTGATATGATGATTTTAAAGGATTCAGAAATTCAGGAACCACTTACTG	423
QY	522	AAACTGTCAAGCTAAGTCAATGCTGATTTGAGGGTATTTCCAAATTTTCAATGAAATGATGCTA	581
Db	424	AAACTGTAAATCACTATTGAATTTGAAAGGATCCCAATATTTAAAGAAATGAAGTCG	483
QY	582	TTAGCACCCGAAGAGCCCATATCAGAAATTTCTGTGATTTTCTGGATTAACATAGCT	641
Db	484	TCAGCACCCAGAAAGCTCATATGAGAGCGCTTCTGTATATTCTGGAAATATGACAGTT	543
QY	642	TACGCTCTACTGGCGTTGGAACTGAAAGTGATCTTCTGATTTCTTGAAGCATGTTG	701
Db	544	TACAGACTTATTAATCTTTGAGAGCTAAAGGTGACCTTCTGTCCTTGAAGTATGG	603
QY	702	AAGCTTTTACACAGCCCTCCAAAGTATCTTAATCAAGTATGATCCACCTTTGTGTA	761
Db	604	AGGGCTTTTATAGGGGCCCAACAGTATCCACGTCAAGTTGATCCACCTTACATTA	663
QY	762	AAGAAAACATCAAGATGATTAATCAATTCGGCGACAATATCAAGATTAGGAGAGGGGTGA	821
Db	664	AGGAATATGTTGAGGAGCTGATTCCTTTTGGGGACAATATCAGGGTGGAAAGGGGGCA	723
QY	822	TGACGTGCAAAATCAAACTGCACTCAATCAGATTTAAGTGGAGATTTCTGTCAATATA	881
Db	724	TGACGTCCAAAGTAAACCTCTGTTTATGAGGCCAATGCTGACATCTCTGTTGTATCA	783
QY	882	CCAGTGGGATTCAAGCTGAGACATAGATTAAGTCCCTCAGAGGACTTGTGTGAACCT	941
Db	784	CCAGTGGGCTATGCTATCGAACATATATCAATAAAGTACTTCAAGGAGAGCGTATTTGGTACC	843
QY	942	TGTTTCAACAGAGTCTGTTTATGGGCTCCGATCAAGTTCTAATGCTCGTGCATAGG	1001
Db	844	TCTTTCATGAGATGACAGAAATGGGCTCAAGTGGAGATGTTGTGTGACGGACATGG	903
QY	1002	CAGTTGCTGCGAGGAAAGTTCCAGAAAGCTTACAGGCTTATCTTGGAAAGACAGAAAA	1061
Db	904	CTGTTGCAAGTAAAGGAGAGTTCCAGAGATTAAGGCCATATGTCCTCCGAAATATAGAGTA	963
QY	1062	AAATTCGTGTAATATGTCGAGTCCCTTGAAGCAATGTTACTACATCAAAAGCTGAG	1121
Db	964	AAATTTCTTGAAGTGGCTGATGCTCTTAACCAATCAATTCGCGGCTTGGCAACA	1023
QY	1122	ATGAGTGTGATGATGCTTGTGACAAAGAGCTGGTGAAGATGCAATAGTGCTGCT	1181
Db	1024	ATGAGAGCTGATCTGCTGCTGACAGAGGCTGCTATGAAATGATATGATATCTGCTC	1083
QY	1182	TAGTTATGACACTTGAAGAAATCTCGAGCTTCAAGTTCGTAGCTAGTATGA	1241
Db	1084	TAGCTCTAAAGTCTGGGAAAGTTTCAAGTCTTCAAAATCAATTCGCGGCTTGGCAACA	1143
QY	1242	TGGAAGATCCGAATGGCGCTGTTTAAAGAAACAAGTGGCAATGCTCTGTCTAG	1301
Db	1144	TGGAAGACCCATTTGTGATGTTTTTGAAGAACTAGATTAACAAGTGAATGCGTCTTAG	1203
QY	1302	AGAAAGCTCATCAACATATAGGGGTACTTCTGATTTTATATCCCGACTGATGAC	1361
Db	1204	AGAAAGATCATCTCCCTGGGGTCTCTCTGATTTTTTTGAAGTCTGACCAAGATGGC	1263
QY	1362	TTGTACAAATAGCTTCACTTGGCATCGTATGTTGAATATGGTCTTCTGCTGAAGGTGGA	1421
Db	1264	TAGTTCAATATGCTTCAATAGCATCAAGTCTGGAATGGTGTGTTTGAAGGGGAAA	1323
QY	1422	AGGAGGCCCGGCAATCAATATGCTATCTTACACAAGGTATCACTGATCAATTCAGAGA	1481
Db	1324	AAGAGGCTAAATATGATGATGCAATCTTGAACAAGTTTATCTTCTGCACTCCGTAAA	1383
QY	1482	CTGTGGGGGTAAATCATATGAGCTTGTGACTTCAAGAGAGAGATTCCTGATTTTGCTTA	1541

Db 1384 ATGTGTCAGAGCTTATGAGCTTGTGACTTCTTAAGAGGAGATCCCGATTTCCTTA 1443
 Qy 1542 AGCTTGATGACGTTATGATCTTGTGATCCAGAGAGAGCAAGAGCTTGTACTCAG 1601
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 Qy 1602 TAAAAAATCTACAAATAATCCCTGCTGTAGTCACTGTGATGATCTGTGATGATG 1661
 Db 1504 TCAAGGATCAACCAAAATTCCTGCTGTAGTCACTGTGATGATGATGATGATGATG 1563
 Qy 1662 TCGCAAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1721
 Db 1564 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1623
 Qy 1722 ATCCAGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1781
 Db 1624 ATCCAGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1683
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 ACCESSION U60267
 VERSION U60267.1 GI:1480669
 KEYWORDS
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1. (bases 1 to 2239)
 REFERENCE Magglio, A., Garcia-Rios, M., Fujita, T., Bressan, R.A., Csonka, L.N.,
 Uchly, R.J., and Hasegawa, M.P.
 TITLE Cloning and partial characterization of PRO2, a second tomato gene
 encoding the enzyme involved in the first two steps of proline
 biosynthesis
 JOURNAL (in) PROCEEDINGS OF THE ASP MEETING;
 (1996)

REFERENCE 2 (bases 1 to 2239)
 AUTHORS Magglio, A., Garcia-Rios, M., Fujita, T., Bressan, R.A., Uchly, R.J.,
 Hasegawa, M.P., and Csonka, L.N.
 TITLE Cloning of tomato PRO2 (Accession No. U7445) and comPRO2 (Accession
 No. U60267) from Lycopersicon esculentum L.: coexistence of
 polyclonal and monoclinal genes which encode the enzymes
 catalyzing the first two steps of proline biosynthesis (PGR96-077)
 JOURNAL Plant Physiol. 112, 862 (1996)
 REFERENCE 3 (bases 1 to 2239)
 AUTHORS Magglio, A., Fujita, T., Garcia-Rios, M., Bressan, R.A., and Csonka, L.N.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUN-1996) Horticulture, Purdue University, 1165
 Horticulture Bldg., West Lafayette, IN 47907, USA
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
Gapop 10⁻⁰, Gapext 1.0

Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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RESULT 1	ABX93778	ABX93778 standard; cDNA, 2571 BP.
ID	ABX93778	
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DT	17-JUN-2003	(first entry)
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DE	Thale cress delta ¹ -pyrroline-5-carboxylate synthetase (P5CS) cDNA.	
XX		
KW	Grass, delta ¹ -pyrroline-5-carboxylate synthetase; P5CS; gene; ss;	
KW	proline dehydrogenase; ProDH; stress tolerance; water tolerance; calli;	
KW	salt stress; salinity tolerance; temperature tolerance; protoplast;	
KW	proline accumulation; thale cress.	
XX		
OS	Arabidopsis thaliana.	
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XX		
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PF	24-DEC-2001; 2001GB-00030946.	
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PR	08-JUN-2001; 2001JP-00174553.	
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PA	(BIO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.	
PA	(INDE-) INDEPENDENT ADMINISTRATIVE INST NAT INST.	
PA	(RIKE) RIKEN KK.	
XX		
PI	Yoshida Y, Shinozaki K;	
XX		
DR	WPI; 2003-203644/20.	
XX	P-PSDB; ABU09030.	
PT	New grass plant overexpressing a P5CS gene from rice, useful for making	
PT	transgenic plants with higher levels of proline accumulating ability, and	
PT	more improved salinity-tolerance, drought-tolerance and low temperature-	
XX	tolerance.	
PS	Claim 2; Page 29-36; 52pp; English.	

XX The invention relates to a grass plant in which a delta¹-pyrroline-5-
CC carboxylate synthetase (P5CS) gene of rice, or a P5CS gene of Arabidopsis
CC thaliana and the antisense gene of a proline dehydrogenase (P5DH) gene
CC of Arabidopsis thaliana, have been introduced in tandemly connected
CC relation to each other. A new method of the present invention is useful
CC for the production of a transgenic rice plant with improved stresses
CC tolerance, especially for water or salt stresses and low temperatures. The
CC invention provides for transgenic plants with a higher level of proline
CC accumulating ability. The invention also relates to a grass plant
CC obtained by introducing a vector comprising a gene of the invention into
CC a calli or protoplast derived from a grass plant, growing the calli or
CC calli or protoplast to obtain a colony and regenerating a plant body from the
CC calli or colony. This sequence represents DNA encoding the thale cress
CC P5CS polypeptide of the invention
XX

Sequence 2571 BP; 698 A; 493 C; 638 G; 742 T; 0 U; 0 Other;

Query Match 100.0%; Score 2571; DB 7; Length 2571;
Best Local Similarity 100.0%; Pred. No. 0;
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 26-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140981P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.

QY 541 TGAATGAGGTTATTCOAATTTTCATGAGATGCTATTTAGACCCGAGAGCCCC 600
 Db 554 TGAATGAGGTTATTCOAATTTTCATGAGATGCTATTTAGACCCGAGAGCCCC 613
 QY 601 AATACAGATTTCTTGTGATTTTCGGGATACAGTACCTAGTGTCTCTAGGCTT 660
 Db 614 ATATCAGATTTCTTGTGATTTTCGGGATACAGTACCTAGTGTCTCTAGGCTT 673
 QY 661 GGAATGAGGTTATTCOAATTTTCATGAGATGCTATTTAGACCCGAGAGCCCC 720
 Db 674 GGAATGAGGTTATTCOAATTTTCATGAGATGCTATTTAGACCCGAGAGCCCC 733
 QY 721 TCAAGGATTCCTAATCTCAAGTATTCOAATTTTCATGAGATGCTATTTAGAC 780
 Db 734 TCAAGGATTCCTAATCTCAAGTATTCOAATTTTCATGAGATGCTATTTAGAC 793
 QY 781 GATTAATTCGCGGAGCAATTCAGATTTAGAGAGGAGGAGTATGATCTGCAAAAGTCAAGC 840
 Db 794 GATTAATTCGCGGAGCAATTCAGATTTAGAGAGGAGGAGTATGATCTGCAAAAGTCAAGC 853
 QY 841 TGAAGTCAATGAGCTTATGCTGGGATTCCTGATCATTAACAGTGGGTATTCAGCTGA 900
 Db 854 TGAAGTCAATGAGCTTATGCTGGGATTCCTGATCATTAACAGTGGGTATTCAGCTGA 913
 QY 901 GAACATATGATTAAGTCTCAGAGAGTACGTTGGACCTTGTTCATCAAGATGCTCG 960
 Db 914 GAACATATGATTAAGTCTCAGAGAGTACGTTGGACCTTGTTCATCAAGATGCTCG 973
 QY 961 TTTATGGGCTCCGATCAAGATTTCTAATGCTGTGACATGCGATGCTGCGAGGAGAG 1020
 Db 974 TTTATGGGCTCCGATCAAGATTTCTAATGCTGTGACATGCGATGCTGCGAGGAGAG 1033
 QY 1021 TTTCAAGAGCTTCAGGCTTATCTTCGAGAGACAGGAGAGAGAGAGAGAGAGAGAG 1080
 Db 1034 TTTCAAGAGCTTCAGGCTTATCTTCGAGAGACAGGAGAGAGAGAGAGAGAGAGAG 1093
 QY 1081 CGATGCCCTTGAAGCAATGTTACTAATCAATCAAGTGAAGTGAATGATGATGCTTC 1140
 Db 1094 CGATGCCCTTGAAGCAATGTTACTAATCAATCAAGTGAAGTGAATGATGATGCTTC 1153
 QY 1141 TGAACAAGAGCTGGGTTGAGAGATCAATGAGTGGCTGCTAGTATGACACCTGAGAA 1200
 Db 1154 TGAACAAGAGCTGGGTTGAGAGATCAATGAGTGGCTGCTAGTATGACACCTGAGAA 1213
 QY 1201 GATCTGAGGCTTCAGCTTCAGTGTGATGATGATGATGATGATGATGATGATGATG 1260
 Db 1214 GATCTGAGGCTTCAGCTTCAGTGTGATGATGATGATGATGATGATGATGATGATG 1273
 QY 1261 TGTTTTAAAGAAACAGAGTGGCAGATGCTTGTCTTAAAGAAACCTCAATCAACCT 1320
 Db 1274 TGTTTTAAAGAAACAGAGTGGCAGATGCTTGTCTTAAAGAAACCTCAATCAACCT 1333
 QY 1321 AGGCGTACTCTGATTTGTTTGAATCCGACCTGATGACCTTGTACAGATGCTTCACT 1380
 Db 1334 AGGCGTACTCTGATTTGTTTGAATCCGACCTGATGACCTTGTACAGATGCTTCACT 1393
 QY 1381 TGCATCCGATGAGGAAATGCTCTTCTGAAAGGTTGAAAGAGAGAGAGAGAGAGAG 1440
 Db 1394 TGCATCCGATGAGGAAATGCTCTTCTGAAAGGTTGAAAGAGAGAGAGAGAGAGAG 1453
 QY 1441 TGCATCTTACAGAGTATGATCTGATTCAGATTCAGAGAGAGAGAGAGAGAGAGAG 1500
 Db 1454 TGCATCTTACAGAGTATGATCTGATTCAGATTCAGAGAGAGAGAGAGAGAGAGAG 1513
 QY 1501 TGAATCTGATCTTCAAGAGAGATGCTGATTTGCTTAAAGTGAATGATGATGATGAT 1560
 Db 1514 TGAATCTGATCTTCAAGAGAGATGCTGATTTGCTTAAAGTGAATGATGATGATGAT 1573
 QY 1561 TCTTGTATCCCAAG 1620
 Db 1574 TCTTGTATCCCAAG 1633
 QY 1621 CCTGTGTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680

Db 1634 CCTGTGTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1693
 QY 1681 GGAATGAGCAAGAGGCAATGTTCTGATGCAAAAGTGGATATCAAGACCTGATATG 1740
 Db 1694 GGAATGAGCAAGAGGCAATGTTCTGATGCAAAAGTGGATATCAAGACCTGATATG 1753
 QY 1741 GATGAGAAACCTTCTTGTGATTAAGATCTTAAGAGAGAAAGTGTGTATGATGAT 1800
 Db 1754 GATGAGAAACCTTCTTGTGATTAAGATCTTAAGAGAGAAAGTGTGTATGATGAT 1813
 QY 1801 TTTGCTCTGAGAGCAATGAGAGTCACTTGTATGATGAGAGAGAGAGAGAGAGAGAG 1860
 Db 1814 TTTGCTCTGAGAGCAATGAGAGTCACTTGTATGATGAGAGAGAGAGAGAGAGAGAG 1873
 QY 1861 GAAATATCCAG 1920
 Db 1874 GAAATATCCAG 1933
 QY 1921 AGTGTAG 1980
 Db 1934 AGTGTAG 1993
 QY 1981 AGACTGATTTGATGAG 2040
 Db 1994 AGACTGATTTGATGAG 2053
 QY 2041 CGCTGCTGTGTTCAAG 2100
 Db 2054 CGCTGCTGTGTTCAAG 2113
 QY 2101 TGAAGAGTGGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
 Db 2114 TGAAGAGTGGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2173
 QY 2161 ATTAATTTCAAG 2220
 Db 2174 ATTAATTTCAAG 2233
 QY 2221 AATGTTTACAG 2260
 Db 2234 AATGTTTACAG 2273
 RESULT 3
 ABZ13586
 ID ABZ13586 standard; DNA; 2154 BP.
 XX
 AC ABZ13586;
 XX
 DT 21-JAN-2003 (first entry)
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1391.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN W0200216655-A2.
 XX
 PD 28-FEB-2002.
 PF 24-AUG-2001; 2001WO-US026685.
 XX
 PR 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T,
 XX

DR WPI: 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.

PS Claim 15; SEQ ID NO 1391; 577bp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array of probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office

XX Sequence 2154 BP; 595 A; 412 C; 562 G; 585 T; 0 U; 0 Other;

Query Match 83.8%; Score 2154; DB 6; Length 2154;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ATGGAGGAGCTAGATCGTTCAAGTCTTTGGCAGAGCGTCAAGATCGTGTAG 166
DB 1 ATGGAGGAGCTAGATCGTTCAAGTCTTTGGCAGAGCGTCAAGATCGTGTAG 60
QY 167 GTTGGGACAGAGTGTCTACTGGAAGGAAAGATTGCTTGTGCTTTAGAGCA 226
DB 61 GTTGGGACAGAGTGTCTACTGGAAGGAAAGATTGCTTGTGCTTTAGAGCA 120
QY 227 CTGTGTGAACAGCTTGGGAAATTAACCTCGATGATTTGGAGATTTGCTCATCT 286
DB 121 CTGTGTGAACAGCTTGGGAAATTAACCTCGATGATTTGGAGATTTGCTCATCT 180
QY 287 GGTGGGATTTGCTTGGGAGCAAGGCTTGTATGACAAATTAAGTATGAGCTTT 346
DB 181 GGTGGGATTTGCTTGGGAGCAAGGCTTGTATGACAAATTAAGTATGAGCTTT 240
QY 347 GGGGATCTTCAGAAAGCTTCAGATGAAATTTGATGGAAGGCTTGTGCTTTGGA 406
DB 241 GGGGATCTTCAGAAAGCTTCAGATGAAATTTGATGGAAGGCTTGTGCTTTGGA 300
QY 407 AGCAGCTTTATGAGCTTACTATGAGACTATGTTTGGACAGCTTGTGAGCGAGCTCAA 466
DB 301 AGCAGCTTTATGAGCTTACTATGAGACTATGTTTGGACAGCTTGTGAGCGAGCTCAA 360
QY 467 CTTCGTGTGATGACAGATGATTTTGAAGCAAGATTTCAAGAACTTAAGAACT 526
DB 361 CTTCGTGTGATGACAGATGATTTTGAAGCAAGATTTCAAGAACTTAAGAACT 420
QY 527 GTCAAGTCTATGATTTGAGGGTATTCATATTTCAATGAGAAATGATGATTAAGC 586
DB 421 GTCAAGTCTATGATTTGAGGGTATTCATATTTCAATGAGAAATGATGATTAAGC 480
QY 587 ACCCGAAGAGCCCATATCAAGATTTCTTGGTATTTCTGGATTAACGATAGCTTAAGCT 646
DB 481 ACCCGAAGAGCCCATATCAAGATTTCTTGGTATTTCTGGATTAACGATAGCTTAAGCT 540
QY 647 GGTCTACAGGCTTGAAGTGAAGCTATCTTCGATTTCTTGAAGGATGTTGAAGCT 706
DB 541 GGTCTACAGGCTTGAAGTGAAGCTATCTTCGATTTCTTGAAGGATGTTGAAGCT 600
QY 707 CTTCACAGAGGCTTCAGATGATCTTAAGTCAAGATTTGATCAACTTTTGTAAAGAA 766
DB 601 CTTCACAGAGGCTTCAGATGATCTTAAGTCAAGATTTGATCAACTTTTGTAAAGAA 660
QY 767 AAACATCAAGATGATTAAGTCAAGATTTGATCAAGATTTGATCAACTTTTGTAAAGAA 826
DB 661 AAACATCAAGATGATTAAGTCAAGATTTGATCAAGATTTGATCAACTTTTGTAAAGAA 720

QY 827 GCAAAAGTCAAGAGCTGCAATGACAGCTTATGCTGGAGATTCCTGTCAATATACAGAT 886
DB 721 GCAAAAGTCAAGAGCTGCAATGACAGCTTATGCTGGAGATTCCTGTCAATATACAGAT 780
QY 887 GGGATTCAGCTGAGAAATAGATTAAGTCTTCAGAGAGCTACGTTGTGAACTTGT 946
DB 781 GGGATTCAGCTGAGAAATAGATTAAGTCTTCAGAGAGCTACGTTGTGAACTTGT 840
QY 947 CATCAAGATGCTGTTTATGAGGCTCCGATCAAGATTTATGCTTCGAGAAATGAGCTT 1006
DB 841 CATCAAGATGCTGTTTATGAGGCTCCGATCAAGATTTATGCTTCGAGAAATGAGCTT 900
QY 1007 GCTGGAGAGAAAGTTCAGAAAGCTTACAGGCTTATCTTGGAAAGACAGAAATTT 1066
DB 901 GCTGGAGAGAAAGTTCAGAAAGCTTACAGGCTTATCTTGGAAAGACAGAAATTT 960
QY 1067 CTGCTTGAATTTGCGGATGCTTCGAGCAAGATTTACTACATCAAGATTTGAGATGAG 1126
DB 961 CTGCTTGAATTTGCGGATGCTTCGAGCAAGATTTACTACATCAAGATTTGAGATGAG 1020
QY 1127 TTAGATGATGCTTTCGCAAGAGGCTGGTGGAGAGTCAATGATGCTGCTTATGTT 1186
DB 1021 TTAGATGATGCTTTCGCAAGAGGCTGGTGGAGAGTCAATGATGCTGCTTATGTT 1080
QY 1187 ATGACAGCTGGAAGATCTCGAGGCTTCGAGCTTCAATTCGTAAGCTTATGAGAA 1246
DB 1081 ATGACAGCTGGAAGATCTCGAGGCTTCGAGCTTCAATTCGTAAGCTTATGAGAA 1140
QY 1247 GATCCATGAGGCTGCTTTTAAAGAAACAGAGGAGGAGATGATGCTTGTGAGAG 1306
DB 1141 GATCCATGAGGCTGCTTTTAAAGAAACAGAGGAGGAGATGATGCTTGTGAGAG 1200
QY 1307 ACCCATCACTTATGAGGCTTCTGATTTGTTTGAATCCGACCTGATGACCTGTA 1366
DB 1201 ACCCATCACTTATGAGGCTTCTGATTTGTTTGAATCCGACCTGATGACCTGTA 1260
QY 1367 CAGATGCTTCACTTCCATCCGTAAGTGAATGCTTTCTGCTGAAAGGTTGAAAGAG 1426
DB 1261 CAGATGCTTCACTTCCATCCGTAAGTGAATGCTTTCTGCTGAAAGGTTGAAAGAG 1320
QY 1427 GCCCGGAGTCAAAAGCTATCTTACAGAGGATCACTGATGCAATTCAGAGCTGTT 1486
DB 1321 GCCCGGAGTCAAAAGCTATCTTACAGAGGATCACTGATGCAATTCAGAGCTGTT 1380
QY 1487 GGGGGTAACTCATGAGCTTGTGACTTCCAGAGAGATTTCTGATTTGCTTAAGCTT 1546
DB 1381 GGGGGTAACTCATGAGCTTGTGACTTCCAGAGAGATTTCTGATTTGCTTAAGCTT 1440
QY 1547 GATGACGTTATGATCTTGTGATCCAGAGAGGAAACAAGCTTGTACTCAGATAAAA 1606
DB 1441 GATGACGTTATGATCTTGTGATCCAGAGAGGAAACAAGCTTGTACTCAGATAAAA 1500
QY 1607 AATTAACAAAATCCCTGTGTAGCTCATGCTGATGAAATCTGATATATGTCAGC 1666
DB 1501 AATTAACAAAATCCCTGTGTAGCTCATGCTGATGAAATCTGATATATGTCAGC 1560
QY 1667 AAGGCTTGTATGAGGATATGCAAGGCAATGATTTCTGATGCAAGATTTGATCA 1726
DB 1561 AAGGCTTGTATGAGGATATGCAAGGCAATGATTTCTGATGCAAGATTTGATCA 1620
QY 1727 GAGGCTTGTATGAGGAAACCTTCTTGTGATTAAGATCTAGAGCAAGATCTGTG 1786
DB 1621 GAGGCTTGTATGAGGAAACCTTCTTGTGATTAAGATCTAGAGCAAGATCTGTG 1680
QY 1787 CTTAATGAGCTTATTTGCTTGTGAGAGCAATGAGTCACTTGTATGAGTGAACAAG 1846
DB 1681 CTTAATGAGCTTATTTGCTTGTGAGAGCAATGAGTCACTTGTATGAGTGAACAAG 1740
QY 1847 GCAAGTATGATCTGAACATACAGAGAGCGGTCACTCAACATGATGATCTGTCCAG 1906
DB 1741 GCAAGTATGATCTGAACATACAGAGAGCGGTCACTCAACATGATGATCTGTCCAG 1800

QY 1907 GCTTGACCTGTTGAAGTTGATAGACGTTTATGCTGCTATGATCACTTACCGAAT 1966
 DB 1801 GCTTGACCTGTTGAAGTTGATAGACGTTTATGCTGCTATGATCACTTACCGAAT 1860
 QY 1967 GGGAGGACACACAGACTGATTTGACAGAGATCAAGAGTTGACAGCTATTCCTT 2026
 DB 1861 GGGAGGACACACAGACTGATTTGACAGAGATCAAGAGTTGACAGCTATTCCTT 1920
 QY 2027 CGCCAAATGATAGCGCTGCTGCTGTTCCAAACGCGACACAAAGATTCTCAGATGTTTC 2086
 DB 1921 CGCCAAATGATAGCGCTGCTGCTGTTCCAAACGCGACACAAAGATTCTCAGATGTTTC 1980
 QY 2087 CGATTGACCTGTTGACAGAGGTTGAGAGCGGCGAGATCCATGCTGCTGTTCA 2146
 DB 1981 CGATTGACCTGTTGACAGAGGTTGAGAGCGGCGAGATCCATGCTGCTGTTCA 2040
 QY 2147 GTGCGGGTGCAGAGATTACTTACACAGAGATGATATGAGAGAGAGAGCAAGTTGTC 2206
 DB 2041 GTGCGGGTGCAGAGATTACTTACACAGAGATGATATGAGAGAGAGAGCAAGTTGTC 2100
 QY 2207 GACGAGACAGATGATTTGTTTACACCCATCAGAGATTCCTCAATCCAGCTTAA 2260
 DB 2101 GACGAGACAGATGATTTGTTTACACCCATCAGAGATTCCTCAATCCAGCTTAA 2154

RESULT 4

ABZ14061

ID ABZ14061 standard; DNA; 2181 BP.

AC ABZ14061;

DT 21-JAN-2003 (first entry)

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1866.

KM Arabidopsis thaliana, plant; gene; stress; transgenic; ds.

OS Arabidopsis thaliana.

XX MO200216655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US026685.

XX 24-AUG-2000; 2000US-0227866P.

XX 26-JAN-2001; 2001US-0264647P.

XX 22-JUN-2001; 2001US-0300111P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

XX Claim 11; SEQ ID NO 1866; 577bp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office

XX Sequence 2181 BP; 624 A; 406 C; 555 G; 596 T; 0 U; 0 Other;
 SQ Query Match 64.3%; Score 1669.8; DB 6; Length 2181;
 Best Local Similarity 86.2%; Pred. No. 0;
 Matches 1848; Conservative 0; Mismatches 297; Indels 0; Gaps 0;

QY 107 ATGAGAGAGTAAATGTTTACAGTCTTTTCCAGAGAGCTCAAGATTCGCTTAA 166
 DB 1 ATAGCGAGATTCAGATGTTTACAGGCTTCCAGAAAGAGCTTAAAGCTATCGTCAAG 60
 QY 167 GTTGGACACAGCTTTGTTACTGAAAAAGTGAAGATTTGCTCTTTAGAGCA 226
 DB 61 GTTGGACCTCAGATTTGTTACTGGAAGAGTGAAGATTTGCTCTTTAGAGCT 120
 QY 227 CTGTGTGAACAGCTTTGGGATTTAACTCGATGATTTGAGGTATTTGCTCATCT 286
 DB 121 ATCTGTGAACAGCTTTGGGATTTAACTCAGATGATTTGAGGTCAATTTGGGTCACT 180
 QY 287 GGTGCGGTTGCTCTTGGACAGCAAGGCTCTTATCGCAATTAATAGCACTTT 346
 DB 181 GGTGCGGTTGCTCTTGGTCAAAAGGCTTCAATCAGCAATTAATAGCACTTT 240
 QY 347 GCGGATCTTGAAGAGCTTCACTGAACTTATGAGAGAGCTTGTGCTGTGAGCA 406
 DB 241 GCAGATTTTACAGAGAGCAAAATGAACTTATGAGAGAGCTTGTGCTGTGAGCA 300
 QY 407 AGCAGCTTTATGCTTATGATGAGATGTTTGAACAAGCTTATGAGAGAGCTTCA 466
 DB 301 AGCAGCTTATGCTTATGATGAGATGTTTGAACAAGCTTATGAGAGAGCTTCA 360
 QY 467 CTCTGTGATGATGACAGTATGTTTGAACAAGATTTTGAACAAGCTTATGAACT 526
 DB 361 ATGCTTGTGACCGATGACAGATTTTGAAGATGAGATTTTGAACAAGCTTATGAACT 420
 QY 527 GTCAAGCTTATGCTTATGAGGTTTATTCGAATTTTCAATGAGATGATGATTAAG 586
 DB 421 GTCAAGCTTATGCTTATGAGGTTTATTCGAATTTTCAATGAGATGATGATTAAG 480
 QY 587 ACCGAGAGAGAGCTTATGAGATGATGATGATGATGATGATGATGATGATGAT 646
 DB 481 ACTGAGAGAGAGCTTATGAGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 647 GCTTATCTGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 706
 DB 541 GCTTATCTGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
 QY 707 CTTTACAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 766
 DB 601 CTTTACAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 660
 QY 767 AAACATCAAGATGATTAATGATGAGGAGCAAAATCAAGATGAGGAGGATGACT 826
 DB 661 AAACATCAAGATGATTAATGATGAGGAGCAAAATCAAGATGAGGAGGATGACT 720
 QY 827 GCAAAAGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 886
 DB 721 GCAAAAGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 887 GGGATTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 946
 DB 781 GGGATTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 947 CATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
 DB 841 CATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 1007 GCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1066
 DB 901 GCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 QY 1067 CTGCTGATATGCTGAGAGAGCTTGAAGCAAAATGATGATGATGATGATGATGAT 1126

Db 961 CTACACACATTCGCCAATGCCCTTGAAGTAAATGAGAAAAAATTAAGTGAATGAT 1020
 Qy 1127 TTAGATGATCTTCTGCAAGAGGCTGGTGGAAAGTCAATGGTGGCTTAACT 1186
 Db 1021 TTAGATGATCTGCAAGAGGCTGGTGAATGAAGAGCTTTGGAGCTGCTTAACT 1080
 Qy 1187 ATGACACCTGGAAGATCTGAGGCTTGCAGCTTCACTTGTAAAGTCAATGATGAA 1246
 Db 1081 ATGAGGCTGGGAAGATCTGAGGCTTGCAGCTTCACTTGTAAAGTCAATGATGAA 1140
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 Db 1141 GATCCAAATGAGCGCTGTTTTAAAGAAAAAGAGGTGGCAGATGATCTTGTGAAGA 1200
 Qy 1307 ACCTCATCAGCTTAAAGGCTACTTCTGATTTGTTGAATCCCGACCTGATGATCTTGA 1366
 Db 1201 ACCCATCAACCAATAGGTTGTTCTGATTTGTTGAATCCCGACCTGATGATCTTGA 1260
 Qy 1367 CAGATAGCTCACTTGCATCCGATGAGAAATGATCTTCTGCTGAAGGCTGAAAGAG 1426
 Db 1261 CAGGATCTTCTGCTTGCATCCGATGAGAAATGATCTTCTGCTGAAGGCTGAAAGAG 1320
 Qy 1427 GCCCGGAGTAAATGCTATCTTACACAGAGTATCTGATGCAATTCAGAGCTGTT 1486
 Db 1321 GCTGCTGATCAATGCTATCTTACACAGAGTATCTGATGCAATTCAGAGCTGTT 1380
 Qy 1487 GGGGGTAACTCATTTGATGATCTTCAAGAGAAAGATTCCTGATTTGCTTAAAGCTT 1546
 Db 1381 GGAGGTAACTCATTTGATGATCTTCAAGAGAAAGATTCCTGATTTGCTTAAAGCTT 1440
 Qy 1547 GATGACGTTATGATCTTGTGATCCCAAGAGAGAACAAAGCTTGTATTCAGATGAA 1606
 Db 1441 GATGACGTTATGATCTTGTGATCCCAAGAGAGAACAAAGCTTGTATTCAGATGAA 1500
 Qy 1607 AATCTCAAAAAATCCCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAC 1666
 Db 1501 AACTGAGAAAAATCCAGTGTAGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAC 1560
 Qy 1667 AAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726
 Db 1561 AAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Qy 1727 GCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
 Db 1621 GCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Qy 1787 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
 Db 1681 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 Qy 1847 GCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1906
 Db 1741 GCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 Qy 1907 GCTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1966
 Db 1801 GCTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 Qy 1967 GAGAGTGCACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2026
 Db 1861 GAGAGTGCACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 Qy 2027 GCGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2086
 Db 1921 GCGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Qy 2087 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2146
 Db 1981 AGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 Qy 2147 GTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2206
 Db 2041 GTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100

Qy 2207 GACGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2251
 Db 2101 GATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2145
 RESULT 5
 AA068841
 ID AA068841 standard; cDNA, 2417 BP.
 AC AA068841;
 XX
 DT 07-APR-1995 (first entry)
 XX
 DE Delta-pyrroline-5-carboxylate synthetase (P5CS) coding sequence.
 XX
 KW Delta-pyrroline-5-carboxylate synthetase; P5CS; proline; crop;
 XX biosynthesis; metabolism; sodium chloride; salt; NaCl; drought; ds.
 OS Vigna aconitifolia.
 XX
 FH Key Location/Qualifiers
 FT CDS 37..2052
 FT /tag= a
 FT /product= "Delta-pyrroline-5-carboxylate synthetase"
 XX
 PN US534923-A.
 XX
 PD 06-SEP-1994.
 XX
 PF 29-SEP-1992; 92US-00953695.
 XX
 PR 29-SEP-1992; 92US-00953695.
 XX
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 XX
 PI Delaney AJ, Verma DPS, Hu CA;
 XX
 DR MPI; 1994-285533/35.
 DR P-PSDB; AAR61135.
 XX
 PT cDNA clone encoding bifunctional enzyme for proline prodn - useful to
 PT prepare transgenic drought resistant plants.
 XX
 PS Claim 1; Fig 1; 17pp; English.
 XX
 CC Delta-pyrroline-5-carboxylate synthetase (P5CS), catalyzes the first two
 CC steps in proline production in plants. By introduction into a plant of a
 CC P5CS cDNA clone, over production of proline is incurred resulting in
 CC increased sodium chloride tolerance and drought resistance. The method
 CC may be used to enhance crop performance under conditions of salt and
 CC drought stress
 CC
 SQ Sequence 2417 BP; 695 A; 445 C; 582 G; 695 T; 0 U; 0 Other;
 Query Match 45.0%; Score 1156.8; DB 2; Length 2417;
 Best Local Similarity 72.7%; Pred. No. 0;
 Matches 1562; Conservative 0; Mismatches 582; Indels 6; Gaps 5;
 Qy 113 GAGCTAATGCTTCACTGCTGCTTTTGCAGAGACGTAACGATGCTGTTAAAGTTGGG 172
 Db 46 GCGGTGATCTCTTCGCGGGGTTCATGAAGACGTAAGCCTGTGATCATCAAGATTGGC 105
 Qy 173 ACAGCAGTTGTTACGTGAAGAGAGTGAAGATGGCTTGTGCTTGAAGACAGTGTGT 232
 Db 106 ACCGCGGTGTACTCGGAGAGAGAGTGAAGATGGCTTGAAGATGGAGCTGTGTGC 165
 Qy 233 GAACAGCTTGCAGAACTTAACCTCGATGATTTAGAGTATTTGCTCATCTGTGTGCG 292
 Db 166 GAGCAGATTAGCACTCACTCTCGATATGCACTTATATCTGCTCTCTGCGCCCC 225
 Qy 293 GTTGTCTTGGAGGCAAGGCTTGTATGACATTAAGCAATTAAGAGCTTGGCGAT 352

Db 226 GTGGATTGAGAGCCAAAGGCTACGTTCCGTAATTAATCAACAGCACTTCCGAC 285
 QY 353 CTTTCAAGAGCTTCAAGCTGAATCTTGAATGAGAGGCTTGTGCTGTTGACAAAGCACT 412
 Db 286 CTTTCAAGAGCTTCAAGCTGAATCTTGAATGAGAGGCTTGTGCTGTTGACAAAGCACT 345
 QY 413 CTTTATGAGCTTCAAGCTGAATCTTGAATGAGAGGCTTGTGCTGTTGACAAAGCACT 472
 Db 346 CTTTATGAGCTTCAAGCTGAATCTTGAATGAGAGGCTTGTGCTGTTGACAAAGCACT 405
 QY 473 GTGATGAGCTTCAAGCTGAATCTTGAATGAGAGGCTTGTGCTGTTGACAAAGCACT 532
 Db 406 GTGATGAGCTTCAAGCTGAATCTTGAATGAGAGGCTTGTGCTGTTGACAAAGCACT 465
 QY 533 TCTATGCTTGAATGAGAGGCTTCAAGCTTGAATGAGAGGCTTGTGCTGTTGACAAAG 592
 Db 466 TCTATGCTTGAATGAGAGGCTTCAAGCTTGAATGAGAGGCTTGTGCTGTTGACAAAG 525
 QY 593 AGAGCCCATATCAGAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 652
 Db 526 AGAGCTTCTTGAAGGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 585
 QY 653 CTGGGCTTGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTT 712
 Db 586 TTAGCCTTGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTT 645
 QY 713 ACAGGCTTGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTT 772
 Db 646 AGTGGCTTGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTT 705
 QY 773 CAGATGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 832
 Db 706 CAGATGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 765
 QY 833 GTGATGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 892
 Db 766 GTGATGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 825
 QY 893 TCAAGCTTGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTT 952
 Db 826 GCACTGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 885
 QY 953 GATGCTTGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTT 1012
 Db 886 GATGCTTGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTT 944
 QY 1013 AGGGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1071
 Db 945 AGGGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1004
 QY 1072 TGAATGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1131
 Db 1005 TGAATGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1064
 QY 1132 TGAATGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1191
 Db 1065 TGAATGAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1124
 QY 1192 ACCTGGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1251
 Db 1125 ACCTGGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1184
 QY 1252 AATGGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1311
 Db 1185 AATGGAAGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1244
 QY 1312 ATCAGCTTGAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1371
 Db 1245 ATCAGCTTGAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1304
 QY 1372 AGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1431
 Db 1305 AGCTTCAAGCTTCTTGGGTAATTTCTGGGTAATGAGAGGCTTGTGCTGTTGAC 1364

QY 1432 GCGATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1491
 Db 1365 GCGATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1424
 QY 1492 TAAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1551
 Db 1425 TAAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1484
 QY 1552 CGTATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1611
 Db 1485 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1544
 QY 1612 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1671
 Db 1545 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1604
 QY 1672 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1731
 Db 1605 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1664
 QY 1732 CTGATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1791
 Db 1665 CTGATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1724
 QY 1792 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1851
 Db 1725 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1784
 QY 1852 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1911
 Db 1785 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1844
 QY 1912 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1971
 Db 1845 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1904
 QY 1972 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2031
 Db 1905 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1964
 QY 2032 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2091
 Db 1965 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2024
 QY 2092 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2150
 Db 2025 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2084
 QY 2151 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2210
 Db 2085 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2141
 QY 2211 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2260
 Db 2142 TGAATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2191

RESULT 6
 AAT77279
 ID AAT77279 standard; cDNA; 2417 BP.
 AC AAT77279;
 XX 25-MAR-2003 (revised)
 DT 26-SEP-1997 (first entry)
 XX
 DE Delta-pyrroline-5-carboxylate synthetase cDNA from mothbean.
 KW P50S; clone pVAB2; bifunctional enzyme; glutamyl kinase;
 KW glutamyl semialdehyde dehydrogenase; proline biosynthesis;
 KW glutamine availability; sodium chloride tolerance; salt tolerance;
 KW drought resistance; transgenic plant; mothbean; ds.

XX OS Vigna aceticifolia.
XX FH Location/Qualifiers
XX Key 37. 2052
XX CDS
FT //tag= a
FT /product= "delta-pyrroline-5-carboxylate synthetase"
FT /note= "Encodes a bifunctional enzyme with both glutamyl-
FT kinase and glutamyl semialdehyde dehydrogenase
FT activities"
FT 2268. 2274
FT polyA_signal
FT //tag= b
XX EN US5639950-A.
XX PD 17-JUN-1997.
XX PD 29-JUN-1994; 94US-00267259.
XX PF 29-SEP-1992; 92US-00953695.
XX PR (OHIS) UNIV OHIO STATE RES FOUND.
XX PA Delauney AJ, Verma DPS, Hu CA;
XX PI WPI; 1997-332099/30.
XX DR P-PSDB; AAM24386.
XX PT Inducing sodium chloride tolerance and drought resistance in plants -
XX using the Vigna aceticifolia delta-pyrroline-5-carboxylate synthetase.
XX PS Claim 3; Fig 1; 19pp; English.
XX CC This sequence is the insert from cDNA clone pVAB2 which encodes the
XX bifunctional enzyme delta-pyrroline-5-carboxylate synthetase (P5CS). The
XX P5CS enzyme catalyses both gamma-glutamyl phosphate and glutamic gamma-
XX semialdehyde production. Transgenic plants transformed with this cDNA
XX overproduce proline. New roots are better protected under salt stress
XX conditions by proline accumulation, and are an important component for
XX overall plant adaptation to cope with drought induced stress. Such plants
XX thus show improved salt tolerance and resistance to drought. The plants
XX can also be engineered to express a glutamine synthetase gene to increase
XX the amount of glutamine available as a substrate for the P5CS. (Updated
XX on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 2417 BP; 695 A; 445 C; 582 G; 695 T; 0 U; 0 Other;
Query Match 45.0%; Score 1156.8; DB 2; Length 2417;
Best Local Similarity 72.7%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 582; Indels 6; Gaps 5;
QY 113 GAGCTAGATCGTTCAGTCTTTTCCAGAGAGCTCAAAAGTATCGTGTAAAGTTGGG 172
DB 46 GGGGAGATCTCTCGGGGGTTCATGAAGAGCGTGAAGCTGTGATCATCAAAAGTTGGC 105
QY 173 ACAGAGATGTTTACGGAAGAGAGAGAGATTTGGCTGTGCTTTAGAGAGAGCTGTGT 232
DB 106 ACCGCGGTGTGACCTCGGAAGAGAGAGAGTTAGCGGTGAAGATTTGGAGCTCTGTGC 165
QY 223 GAAACAGCTTGCAGATTAATTAATCGATGATTTAGATTTAGTGTCTATCTGTGCG 292
DB 166 GAGCAGATTAATTAATTAATCGATGATTTAGATTTAGTGTCTATCTGTGCG 225
QY 293 GTTGTCTTGGAGAGAGAGAGAGAGATTTAGATTTAGTGTCTTGTGAGAGAGAT 352
DB 226 GTTGTCTTGGAGAGAGAGAGAGAGATTTAGATTTAGTGTCTTGTGAGAGAGAT 285
QY 353 CTTTGAAGAGAGAGAGAGAGAGATTTAGATTTAGTGTCTTGTGAGAGAGAT 412
DB 286 CTTTGAAGAGAGAGAGAGAGAGATTTAGATTTAGTGTCTTGTGAGAGAGAT 345
QY 413 CTTTGAAGAGAGAGAGAGAGAGATTTAGATTTAGTGTCTTGTGAGAGAGAT 472

DB 346 CTGATGCTCTTCAAGATAGCTGTTCATCTAGCTGATGTGACATGCGCTTCTT 405
QY 473 GTGAATGACAGTATTTTAAAGACAGAGATTTCCAGAGAGAGATTTAAATGAACTGTCAAG 532
DB 406 GTGACGATTAAGATTTTTCGATATAGAGATTTCCAGAGAGAGATTTTCTGAGAGCTGTGAAG 465
QY 533 TCTATGCTTGAATTTAGAGAGATTTTCAATTTTCAATGAGATTTGATTTAGACCCGCA 592
DB 466 TCGCTTTGGAGCTGAGAGATTTTTCGATTTTTCGATTTTCAATGAGATTTGATTTAGACAG 525
QY 593 AAGAGCCCATTAACAGATTTCTTGTGATTTTCTGAGATTAACAGATTTAGCTTCTCTA 652
DB 526 AAGGCTCCCTATGAGATTTCTTGTGATTTTCTGAGATTTTCTGAGATTTTCTGAGATTT 585
QY 653 CTGAGCTTGAAGAGAGAGAGAGAGATTTTCTGAGATTTTCTGAGATTTTCTGAGATTT 712
DB 586 TTAGCTTTGAGATTAAGAGAGAGAGATTTTCTGAGATTTTCTGAGATTTTCTGAGATTT 645
QY 713 ACAGAGCCCTCCAGATGATCTTCAATGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 772
DB 646 AGTGCCTCCAGATGATCTTCAATGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 705
QY 773 CAAGATGATTTCAATTTGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 832
DB 706 CAGATGATTAATTTCTTGTGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 765
QY 833 GTCAAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 892
DB 766 GTAAAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 825
QY 893 TCAAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 952
DB 826 GCACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 885
QY 953 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1012
DB 886 GAT 944
QY 1013 AGGAGAGATTTCAAGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 1071
DB 945 AGGAGATTTCAAGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 1004
QY 1072 TGAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1131
DB 1005 TAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1064
QY 1132 TGTAGCTTCTGAGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 1191
DB 1065 TGTAGCTTCTGAGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 1124
QY 1192 AACTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1251
DB 1125 AACTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1184
QY 1252 AATGAGAGAGATTTTAAAGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 1311
DB 1185 AATGAGAGAGATTTTAAAGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 1244
QY 1312 ATCAAGATTTGAGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 1371
DB 1245 ATCTGCTTTGAGAGAGAGAGAGAGATTTTCAATGATTTTCTGAGATTTTCTGAGATTT 1304
QY 1372 AGCTTCACTTGCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1431
DB 1305 AGCTTCACTTGCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1364
QY 1432 GCGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1491
DB 1365 GCGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1424
QY 1492 TAAACTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1551
DB 1425 AAAACTTATGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1484

OY	527	GTCAAGCTAATGCTTGAATTTGAGGGTATATCCAAATTTTTCATGAGATGATGCTAATAGC	586
Db	519	GTTGAGTCATTAATTGATCTTTAAAGTTATACCAATATTTTAAATGATGATCCATCAGC	578
OY	587	ACCCGAAGAGCCCAATATCAGAAATTCCTCTGGTATATTTCTTGGATTAACGATAGCTTAGT	646
Db	579	ACTAGAAAGGCTCATATGAGGAATTCATCTGGTATATCTGGATTAATGACAGTTTAGCA	638
OY	647	GCTCACTGCGGCTTGGAACTGGAAAGCTGATCTTCTGATTTCTTGGACGAAATGTTGAAGT	706
Db	639	GGACTGTTGSCACTGGAACTGAAAGCTGATTCCTTAATTCGCTCACTGATGTGCGATGGG	658
OY	707	CTTTACACAGCCCTCCAGATGATCTTAATCTCAAGTGTATCCACACTTTTGTAAAGAA	766
Db	699	TTGTAATAGTGCTCACCAAGTGAACCAATCATCAAAATATCAACACTATATTAAGAA	758
OY	767	AAACATCAAGATGAGATTAATCATTTGGGCGACAAATCAAGATTAAGGAGAGAGGGGATACCT	826
Db	759	AAGCATCGACAAGAAATCATCTTTGGAGACAAATCTGTAAGGTAAAGAGGATACACA	818
OY	827	GCAAAAGTCAAAGCTGACAGTCAATGACGCTTAATCTGGGATTCCTGTCAATCATACCACT	886
Db	819	GCAAAAGTGAAGGCTGCTGCTTTGGCTTCAAAATAGCGCACACCTGTGGTTATTAACAAGT	878
OY	887	GGGTATTCAGCTGAGAACATAGATTAAGTCTCTCAGAGGACTACGTGTTGGAACCTTGTT	946
Db	879	GGGTTTGAATAATCGGACGATCTTAAAGTTCCTCATGGGGAATAAATTTGTAACCTCTTT	938
OY	947	CATCAAGATGCTCGTTTATAGGGGCTCCGATCAAGATTCATATGCTCGGACATGAGCAGTT	1006
Db	939	CACAAAGATGGAATTTGTGGAAATCATCTAAGATGTTAGTACTCGTAGATGCGCTGTT	998
OY	1007	GCTGCGAGGAGAAAGTTTCAGAAAGCTTCAGGCTTAATCTTCGGAAGACAGAAAAAATTT	1066
Db	999	GCCGCAAGAGATTTGTTCAAGCATCTACAGATTTGTTCATCAGAGGAAACGAAAAAGATA	1058
OY	1067	CTGCTGTATATTGCCGATGCCCTTGAACCAATGTTACTAATCAATCAAGCTGGAATAGAG	1126
Db	1059	TTGCTAGATGTTCAGATGCTTTGGAGCAAAATGAGATTTAAATAGGCTCTGAAATGAA	1118
OY	1127	TTAGATGATGCTTCGCAACAAGAGCTGGGTGGAAGATCAATGTTGGCTCGCTTAGTT	1186
Db	1119	GCTAGTATAGCTGCGGCCCAAGTTGCTGATATAGGAAGCCTTTGGTGTAGATTGACT	1178
OY	1187	ATGACACTCGGAANAATCTCCAGCTTCGACCTTCAGTTCGTAACTAGCTGATATAGAA	1246
Db	1179	ATPAAACCAAGAAATATGACAAGCCTTGCAAATATATTCGTATCCTTGGCAAAATAGAA	1238
OY	1247	GATCCAAATCGGCGCTGTTTAAAGAAACAGAGGTGCGAGATGTCCTTGTAGAGAG	1306
Db	1239	GACCTTAATTAACCAATACTTAAAGAAGACAGGTGTGATGATTTAGTTCTTGAAGAA	1298
OY	1307	ACCTCATCCACTTAGGCGTACTTGTATGTTTGAATCCGACCTGATGCACTTGTA	1366
Db	1299	AATCTTGGCCATTTAGGTGTCTCTTAATGTTTGTGATCCCACTCGATGCCCTTGTT	1358
OY	1367	CAGATAGCTTCCTTGCATCCGCTGTGGAATGCTCTTCGCTCAAGAGGTGAAAAAGAG	1426
Db	1359	CAGATTCATCTTTGGCAATTCAAAGTGTATGCTTCTTCCTTAAAGTGGAAAAA	1418
OY	1427	GCCCGCGAATCAATATGTAATCTTACACAAGGTGATCACTGATGCAATTCAGACATGTT	1486
Db	1419	GCTATCAGATCAAAACGATATTGTCATAAGGTTTAACTGAATGCAATTCCTGTATGTT	1478
OY	1487	GGGGGTAATCTATGAGATGTTGATCTTCAAGAGAAGATCCGATTTGGTTAAGCTT	1546
Db	1479	GGGGAATAATTAATGGCTTGTATCAACTAAGATGAGATGCAATTTGCTAAAGCTT	1538
OY	1547	GATGACGTAATGATCTTGTGATCCCAAGAGAACCAACACTTGTATCTCAATPAAA	1606
Db	1539	GATGATGTCATTTGATCTTGCTCACTCCAAAGAGAAATTAACCTGTCTCAATCAAG	1598
OY	1607	AATACTACAAAAATCCCTGTGTAAGTCACTGATGAAATGTGCATGTATATGTCCAG	1666

Db		1599	GCGCAACTAAGATTCCTGTTCTTGGGCACGTGATGTGTAATGCCAGATATATTGAC	1658
Oy		1667	AAGCCTTGATACCGATATATGGCAAAGCCGATAGTTTCTGATGCAAGTTGACTATCCA	1726
Db		1659	AAATCACCTGACATGATGATATGGCAAAACTTAATGTATATGATGTGCAAAAACGTATTACC	1718
Oy		1727	GCAGCCTGATATGGCATGGAACCCCTTGTGTGATATAAGATCTAGAAGCAAGATGCTGTG	1786
Db		1719	GCAGCCTGCAATGCAATGAGAACCTTACTGATTCATTAAGATCTTAGAAGAGTCCAGGC	1778
Oy		1787	CTTAATAGACTTAATTTTTGCTCTGCGACAGCAATGAGTCACTTTGTATGTGTGACCAAG	1846
Db		1779	CTTAGACACATATTATAGACACTAAAAACAAGAGATTAATATTATGTGGGACCTATT	1838
Oy		1847	GCAGTAAAGATTAAGACATACCAAGAGACCGGCTATTCAACATGATGACTGTGCCAAG	1906
Db		1839	GCGCACAAAGCTCTGGGATTTCCAAAAGCTGTTTCATTTCATCATGAGTANGTCTATG	1898
Oy		1907	GCTTGCACTGTGTAAGTTGTAGAAAGGCTTTATGTCATATGATCAATTCAACGCAT	1966
Db		1899	GCTTGCACTGTGATGTTGTTGATGATGTTCAATCAGCAATTGACATATTCAATGTTAT	1958
Oy		1967	GGAGTGCACACACAGACTGATTTGTGCACAGAGATCAAGAA GTTGAGAGCTATTGCTT	2026
Db		1959	GGAGTCTCTATACAGATTGTATGTCACTACATATATATAGTAGAGACACTTTTCTA	2018
Oy		2027	CGCCAGTGAATACCGCTGCTGTCTCCACAAACCAGCAACAAGTTCTCATGTGTTTC	2086
Db		2019	CGCAGATGTAATATGTCGTCTGTATTTCAATATGCCAAGTAGAATCTCTGATGGGCT	2078
Oy		2087	CGATTGACTTGTGTGCAGAGGTGSGGTAACACCGGCAAGATTCATGCTGTGTTCCA	2146
Db		2079	CGTTTGGATTGGGTGCTGAGGTGGATMAAGCAAGGCGTATCCATGCCCCGTGACCA	2138
Oy		2147	GTCGGGGTCGAAGGATTACTTACAAACGAGATGATTAATGAGAGGAAAAGCAAGTTGC	2206
Db		2139	GTCGGGTGTAAGGTCTCTTAACATACAGATGATCTTGCAAGAGACGTGGCAAGTGTG	2198
Oy		2207	GACGAGACAAATGGAATTTGTTTACACCCATCAGACATTTCCATCCAA	2254
Db		2199	AATGGTGCAGAGATGTGTTACACCCATATGAGTCTTCTTGCAA	2246
<hr/>				
RESULT 8				
AAV15744				
ID	AAV15744	standard; cDNA to mRNA; 2549 BP.		
XX	AAV15744;			
XX	AAV15744;	(first entry)		
DE	Rice delta-1-pyrroline-5-carboxylate synthase cDN.			
KM	Rice; delta-1-pyrroline-5-carboxylate synthase; salt resistance;			
XX	moisture loss; ds.			
OS	Oryza sativa.			
XX				
XX	Key	Location/Qualifiers		
FT	CDS	99..2249		
FT	/tag= a			
FT	/product= "delta-1-pyrroline-5-carboxylate_synthase"			
PN	JF10057069-A.			
PD	03-MAR-1998.			
PF	22-AUG-1996;	96UP-00221465.		
PR	22-AUG-1996;	96UP-00221465.		
XX				
PA	(HITA) HITACHI LTD.			

XX WPI: 1998-210402/19.
 DR P-PSDB; AAM47389.
 XX
 PT Rice delta-1-pyrroline-5-carboxylate synthase gene - useful for providing
 salt resistance and preventing moisture loss in plants.
 PS Claim 1; Page 3-9; 9pp; Japanese.
 XX
 CC The present sequence encodes rice delta-1-pyrroline-5-carboxylate
 synthase, which can be used to provide salt resistance and prevent
 moisture loss in plants, improving crop yield
 CC
 XX Sequence 2549 BP; 719 A; 453 C; 648 G; 729 T; 0 U; 0 Other;

Query Match 41.3%; Score 1062.8; DB 2; Length 2549;
 Best Local Similarity 69.4%; Pred. No. 3.4e-296;
 Matches 1445; Conservative 0; Mismatches 637; Indels 0; Gaps 0;

QY 173 ACAGAGTTGTTACGGAAGAGTGGAGATTGCTCTTGTCTTTAGAGCACTGTGT 232
 DB 165 ACTGCGATTGCTCCAGACAGATGGAGATTGCTTGGCAGGGTTGAGCTCTGTGC 224
 QY 233 GAACACCTCGGAATTAACCGATGGATTGAGGATATTGGTGTCACTGTGCG 292
 DB 225 GAGCAGGTTAAGAACTGAACTCTTTAGATACGAGATGATTTGTCACTCAAGTCT 284
 QY 293 GTTGTCTTGGCAGGCAAGGCTTGTATCGACATTAAGTCAATGACGCTTTCGGAT 352
 DB 285 GTTGGATGGGGGACAGCGACTTAGTACCGGAAGCTTGTCAATAGCAGCTTTCGAT 344
 QY 353 CTTCAGAACCTCAGACTAATCTGATGGAGAGGCTTGTCTGTGTGTGCAAAAGCAT 412
 DB 345 CTGCAAAACCCACAGATGAGTTAAGTGAAGGCTTGTGCGCTGTGTGTCAGTGA 404
 QY 413 CTATGCTTACTATGAGACTATGTTTGAACAGCTTGTATGACGCGACCTCACTTGTG 472
 DB 405 CTGATGCTCTTTAGATATGTTGTTTAAACAAGTGTCTGTCACTCACTTCTT 464
 QY 473 GTGATGACAGATGTTTGAAGCAAGATTTCAAGAGCACTTAATGAACCTGTCAAG 532
 DB 465 GTCAACGAGATGATTTAGAACCCCAAGTTCGCGAGCACTCACTGAACCTGTGAG 524
 QY 533 TCTATGCTTATTTAGGCTTATTCATTTCAATGAGATGATGATTAAGCAACCGCA 592
 DB 525 TCAATTTATGATCTTAATGATTAACCAATTTAATGAATGATGATCACTGACCTGA 584
 QY 593 AAGGCCCATATCAGATTTCTGTGATTTTCTGGATTAACGATAGCTTACGCTCTTA 652
 DB 585 AAGGCTCCATATGAGATTCATCTGTATATCTGGGATTAATGACAGTTTACAGGACTG 644
 QY 653 CTGCGCTTGAAGCTGAAGCTGATCTTCTGATTTCTTCTGAGGATGTTGAAGGCTTAC 712
 DB 645 TTGGCACTGAACTGAAGCTGATCTCTTATTTCTGCTCACTGATGATGATGATGAT 704
 QY 713 ACAGGCTTCCAGATGATCTTAATCTAAAGTTGATCACTTTTGTAAAGAAAACAT 772
 DB 705 AGTGTGTCACCAAGTGAACATCAATAAATCATACACTTAATTAAGAAAAGAT 764
 QY 773 CAGATGAGATTAATTCGCGCAGCAATGAAGTTAGGAGAGGGGGATGATGATCAAA 832
 DB 765 CAGCAAAATCACTTTTGAAGCAATCTCGTGTGAGAGAGGCTGACAGCAAAA 824
 QY 833 GTCAAAAGCTCAGTCAATGAGTTATGCTGGGATTCCTGTCAATTAACAGGGGAT 892
 DB 825 GTGAAGGCTGTCTTGGCTTCAATTAACGGGACACCTGTGTATTAACAAGGGGTT 884
 QY 893 TCGCTGAGAACTAATTAAGTCTCAGAGACTACGTTGGAACCTGTTTATGATA 952
 DB 885 GAAATCGAGCACTTTAAATTTTCAATGGGAAAAAATGTTGATCTCTTTCAAG 944
 QY 953 GATGCTGTTTATGAGCTCGATCAGATTTCAATGCTCGTGAAGTGCAGTTGCTCG 1012

DB 945 AATGCAATTTTGGGAATCATCTAAGATGTTAGTACTCTGATGATGCTGTGCCGA 1004
 QY 1013 AGGAAAGTTCCAGAAAGCTTCAGGCTTATCTTCGAAAGCAGGAAAAATTCGCTT 1072
 DB 1005 AGAGATTGTCAAGGCACTTACAGAAATTTGTCACTGAGAGAACGAAAAAATTTGCTA 1064
 QY 1073 GATATGCGCATGCTCCCTTGAAGCAATGTTACTACATCAATCAAGCTGAGATGATGAT 1132
 DB 1065 GATGTTGACATGCTTTTGAAGCAATGAGATTTAATAAAGCTGAGATGAGCTGAT 1124
 QY 1133 GTAGCTTTCAGAAAGAGGCTGGGTTGGAAGATCAATGTTGCTGCTTACTAGTAA 1192
 DB 1125 GTAGCTGCGGCCCAAGTGTCTGATATGAGAAAGCTTTGGTGTCTAGATTGACTATPAA 1184
 QY 1193 CTTGAAAGATCTCGAGCTTTCAGCTTCAATGCTTACCTGATGATGATGAGATGCA 1252
 DB 1185 CAGGAAAGATACCAAGCTTCGCAAAATCTATTCGATACCTTGCATATGAGAACCTC 1244
 QY 1253 ATGCGCGGTGTTTAAAGAAACAGAGGTGCGAGATGTTCTTGTCTTAAGAAAGCTCA 1312
 DB 1245 ATAAACAGATACCTTAAAGAAACAGAGGTGCTGATGATTTAGTTCTTGAAGAAACATCT 1304
 QY 1313 TCACATTAAGGCTTACTTCTGATTTGTTTGAATCCGACCTGATGCACTTGTACAGATA 1372
 DB 1305 TGCCATTAAGTGTCTTCTTAATTTGTTTGAATCCGACCTGATGCTTGTGATGAT 1364
 QY 1373 GCTTCACTTGCATCCGATGAGAAATGCTCTTCTGCTGAAGGTTGAAGAGCCCG 1432
 DB 1365 GCATCTTTGGCAATGGAAGTGTAAATGCTTCTCCTAAAGGTGGAAGAAAGATATC 1424
 QY 1433 CGATCAAAATGCTATCTTACCAAGATGATCACTGATGCAATTCAGACCTGTGGGAGT 1492
 DB 1425 AGATCAAAACAGATTTGCAATAGGTTATATCACTGATGCTATCTCTGTATGTTGTTGA 1484
 QY 1493 AAATCAATGAGCTTGTGATCTTCAAGAGAAAGATCTCTGATTTGCTTAAGCTTGTATGAC 1552
 DB 1485 AAATTAATGCTTGTATCAATAGATGATGATGATGATGATGATGATGATGATGAT 1544
 QY 1553 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1612
 DB 1545 GTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1604
 QY 1613 ACAAAATCCCTGTGCTAGTATGCTATGATGATGATGATGATGATGATGATGATGAT 1672
 DB 1605 ACTAATGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1664
 QY 1673 TGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1732
 DB 1665 GCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1724
 QY 1733 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1792
 DB 1725 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1784
 QY 1793 GAGCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1852
 DB 1785 GACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1844
 QY 1853 AAGTACTGAACATACAGAGACCGCTTCTTGTGATAGATCTGAGAGATGCTGTGCTTGA 1912
 DB 1845 AAAGCTGTGGGATTTCCAAAGCTGTTTCACTTCACTCAAGATATGTTATGCTGCTGCTG 1904
 QY 1913 ACTGTTAAGTTGTAGAAAGCTTTTATGCTGTATGATGATGATGATGATGATGATGATGAT 1972
 DB 1905 ACTGTTAAGTTGTAGAAAGCTTTTATGCTGTATGATGATGATGATGATGATGATGATGAT 1964
 QY 1973 GCAACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2032
 DB 1965 GCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2024
 QY 2033 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2092
 DB 2025 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2084

QY 2093 GCACCTGTCAGAGGTGGGAGTAAACACGAGGAGATCCATGCTCGTGTCCAGTCCG 2152
DB 2085 GAGTTGGTGGCTGAGGTTGGCATACGACAGGAGCGATCATGCCCGTGCACGATGGGT 2144
QY 2153 GTGGAAGATCTACTTCAACGAGATGATATGAGGAAAGCAACTTGTCCACGGA 2212
DB 2145 GTTGAAGGCTCTCTTAACACGATGATCTTGGCAGGAGCGTGGGCAAGTGTGAATGAT 2204
QY 2213 GACATGATGATTTTACACCCATCAGACATTCCTCCATCCAA 2254
DB 2205 GACAGAGATGCTGTACACCCATTAAGATGCTTCTTCCAA 2246
RESULT 9
AAC44944
ID AAC44944 standard; DNA; 1343 BP.
XX
AC AAC44944;
DT 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 44716.
DE
XX Hybridization assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
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PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
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PR 18-MAY-1999; 99US-0134768P.
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PR 03-JUN-1999; 99US-0137528P.

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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
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PR 01-JUL-1999; 99US-0141842P.
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PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
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PR 13-JUL-1999; 99US-0142977P.
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PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
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 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
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 PR 04-OCT-1999; 99US-015717P.
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 PR 22-OCT-1999; 99US-0160989P.
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 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 35.0%; Score 900.4; DB 3; Length 1343;
 Best Local Similarity 86.8%; Pred. No. 2,3e-249;

Matches 991; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
 1110 TCAAGCTGAGAAATGAGTATGATGATCTTGCACAGAGGCTGGTGGAAAGTCAA 1169
 Db 1 TTAAGCTGAGAAATGATTAATGATGATCTTGCACAGAGGCTGGTGGAAAGTCAA 60
 1170 TGGTGGCTCGCTTAATGATTAATGACACCTGGAAAGATCTTCGACCTTCGATTCGTA 1229
 Db 61 TGGTGGCTCGCTTAATGATTAATGACACCTGGAAAGATCTTCGACCTTCGATTCGTA 120
 1230 AGCTAGCTGATATGAGAAATGCAATCGCCGCTTTTAAAGAAACAGAGTGGCAATG 1289
 Db 121 AGCTAGCTGATATGAGAAATGCAATCGCCGCTTTTAAAGAAACAGAGTGGCAATG 180
 1290 GTCTTGTCTTAAGAGAAAGCTCATCACATTAGGCGTACTTCTGATTTTGGATCCC 1349
 Db 181 ATCTTATTTTAAAGAAAGCTCATCACATTAGGCGTACTTCTGATTTTGGATCCC 240
 1350 GACCTGATGACCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1409
 Db 241 GACCTGATGACCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 1410 TGAAGGTTGAAAGAGAGGCGCGGATCAATGCTATCTTACCAAGTGTATCATGATG 1469
 Db 301 TGAAGGTTGAAAGAGAGGCGCGGATCAATGCTATCTTACCAAGTGTATCATGATG 360
 1470 CAATTCAGAGACTCTTGGGGGTAACTCATTTGACTTGTGATCAAGAGAGAGATTC 1529
 Db 361 CAATTCAGAGACTCTTGGGGGTAACTCATTTGACTTGTGATCAAGAGAGAGATTC 420
 1530 CTGATTTGCTTAAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1589
 Db 421 CTGATTTGCTTAAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 1590 TTGTTACTGATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1649
 Db 481 TTGTTACTGATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 540
 1650 GTGATGATATGTCAGCAAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 1709
 Db 541 GTGATGATATGTCAGCAAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 600
 1710 CAAAGTTGACATTCAGCAAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 1769
 Db 601 CAAAGTTGACATTCAGCAAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 660
 1770 TAGAGCAAGATGCTGCTTAATGAGCTTATTTTGTGTCAGAGCAATGAGTCACTT 1829
 Db 661 TAGAGCAAGATGCTGCTTAATGAGCTTATTTTGTGTCAGAGCAATGAGTCACTT 720
 1830 TGTATGTTGACCAAGGCAAGTAAAGTAACTGACATACCAAGCAAGCAAGCTTCAATCAAC 1889
 Db 721 TGTATGTTGACCAAGGCAAGTAAAGTAACTGACATACCAAGCAAGCAAGCTTCAATCAAC 780
 1890 ATGATGATGTCGCAAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1949
 Db 781 AAGATGATGTCGCAAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 1950 ATTCATTTACCAAGCAAGTAAAGTAACTGACATACCAAGCAAGCAAGCTTCAATCAAC 2009
 Db 841 ATTCATTTACCAAGCAAGTAAAGTAACTGACATACCAAGCAAGCAAGCTTCAATCAAC 900
 2010 TTGCAAGCTATTTCTTGTGCAAGTAAAGTAACTGACATACCAAGCAAGCAAGCTTCAATCAAC 2069
 Db 901 TTGCAAGCTATTTCTTGTGCAAGTAAAGTAACTGACATACCAAGCAAGCAAGCTTCAATCAAC 960
 2070 GATTCCTGATGATTTTCTTGTGCAAGTAAAGTAACTGACATACCAAGCAAGCAAGCTTCAATCAAC 2129
 Db 961 GATTCCTGATGATTTTCTTGTGCAAGTAAAGTAACTGACATACCAAGCAAGCAAGCTTCAATCAAC 1020
 2130 TCCATGCTGCTGTCAGTGGGCTGCAAGATTAATTAATCAAGATGATTAATGAGAG 2189
 Db 1021 TTGATGCTGCTGTCAGTGGGCTGCAAGATTAATTAATCAAGATGATTAATGAGAG 1080

QY 2190 GAAAGACAAAGTGTGACGAGACATGAAATTTTACACCCCATCAGACATTCCA 2249
 DB 1081 GAAAGACAAAGTGTGACGAGACATGAAATTTTACACCCCATCAGACATTCCA 1140
 QY 2250 TC 2251
 DB 1141 TC 1142

RESULT 10
 ABX57016
 ID ABX57016 standard, DNA, 564 BP.
 AC ABX57016;
 DT 20-FEB-2003 (first entry)
 XX Arabidopsis thaliana polynucleotide #368.
 DE Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;
 KW genetic modification; environmental stress; disease resistance;
 KM fungicide; insecticide; stress tolerance.
 OS Arabidopsis thaliana.
 XX US2002040489-A1.
 FN 04-APR-2002.
 PD 26-JAN-2001; 2001US-00770152.
 PF 27-JAN-2000; 2000US-0178503P.
 ER (GORL/) GORLACH J.
 PA (ANYV/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYV/) YU Y.
 PA (RAME/) RAMEKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICK/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameka JG, Page A, Mathw AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX MPI, 2003-110410/10.
 PT Novel Arabidopsis thaliana nucleic acid useful for identifying homologous
 PT or related genes, and to create genetically modified and transgenic
 PT organisms, such as plant cells and plants.
 PS Claim 1; SEQ ID NO 368; 45bp; English.
 CC The invention relates to Arabidopsis thaliana nucleic acid sequences. The
 CC DNA sequences and the polypeptides they encode are useful for identifying
 CC homologous or related genes, for producing compositions that modulate the
 CC expression or function of the polypeptides, for mapping functional
 CC regions of the protein, in diagnosis, for studying associated
 CC physiological pathways, for genetic manipulation of cells, preferably

CC plant cells, in screening assays of various plant strains to determine
 CC the strains that are capable of withstanding a particular disease or
 CC environmental stress, for enhancing or inhibiting production of
 CC biosynthetic products in plants and to create genetically modified and
 CC transgenic organisms, such as plant cells and plants. Transgenic plants
 CC are useful for introducing or improving disease resistance and stress
 CC tolerance in plants, screening biologically active agents, such as
 CC fungicides and insecticides, and for elucidating biochemical pathways.
 CC Sequences ABX56649-ABX57647 represent Arabidopsis thaliana
 CC polynucleotides of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 564 BP, 151 A, 112 C, 139 G, 162 T, 0 U, 0 Other;

Query Match 21.6%; Score 555.6; DB 7; Length 564;
 Best Local Similarity 99.3%; Pred. No. 8,1e-150;
 Matches 558; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1278 AGTGGCAGATGCTGCTTGTAGAGACCTCATACCATAGAGGCTTCTGATTTG 1337
 DB 3 ACGGCTCCGATGCTTGTCTTAGAGACCTCATACCATAGAGGCTTCTGATTTG 62
 QY 1338 TTTTGAATCCCGACCTGATGCACTTGTACAGATAGCTTGCATCCGATGGA 1397
 DB 63 TTTTGAATCCCGACCTGATGCACTTGTACAGATAGCTTGCATCCGATGGA 122
 QY 1398 ATGCTCTTCTGCTGAAGGCTGGAAGAGCCCGCGGANTCAATGCTTTCACAGG 1457
 DB 123 ATGCTCTTCTGCTGAAGGCTGGAAGAGCCCGCGGANTCAATGCTTTCACAGG 182
 QY 1458 TGATCACTGATGCAATTCAGAGACTGTGGGGTAACTCATTTGATGACTTGA 1517
 DB 183 TGATCACTGATGCAATTCAGAGACTGTGGGGTAACTCATTTGATGACTTGA 242
 QY 1518 GAGAGAGATTCCTGATTTGCTTAAAGCTTGATGACCTTATGATCTTGTATCCCAAG 1577
 DB 243 GAGAGAGATTCCTGATTTGCTTAAAGCTTGATGACCTTATGATCTTGTATCCCAAG 302
 QY 1578 GAAGCAACAAGCTTGTACTAGATTAATAAATACTAATAAATCCCTGTAGTATG 1637
 DB 303 GAAGCAACAAGCTTGTACTAGATTAATAAATACTAATAAATCCCTGTAGTATG 362
 QY 1638 CTGATGATTCGTGATGATATATGTCGACAAAGCTTGTGATCCGATATGCAAGGCA 1697
 DB 363 CTGATGATTCGTGATGATATATGTCGACAAAGCTTGTGATCCGATATGCAAGGCA 422
 QY 1698 TAGTTTCTGATGCAAGTGTGACTATCCAGAGCCTGTAATGCGATGAAACCTTCTTG 1757
 DB 423 TAGTTTCTGATGCAAGTGTGACTATCCAGAGCCTGTAATGCGATGAAACCTTCTTG 482
 QY 1758 TGCAATGAGATCTAGAGCAAGATGCTGTGTAATGAGCTTATTTTGTCTGAGAGCA 1817
 DB 483 TGCAATGAGATCTAGAGCAAGATGCTGTGTAATGAGCTTATTTTGTCTGAGAGCA 542
 QY 1818 ATGAGTCACTTGTGATGATG 1839
 DB 543 ATGAGTCACTTGTGATGATG 564

RESULT 11
 ABX56679
 ID ABX56679 standard, DNA, 594 BP.
 AC ABX56679;
 DT 20-FEB-2003 (first entry)
 XX Arabidopsis thaliana polynucleotide #31.
 DE Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;
 KW genetic modification; environmental stress; disease resistance;
 KM fungicide; insecticide; stress tolerance.

XX Arabidopsis thaliana.
 OS US2002040489-A1.
 XX 04-APR-2002.
 XX 26-JAN-2001; 2001US-00770152.
 XX 27-JAN-2000; 2000US-0178503P.
 XX (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICK/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX WPI; 2003-110410/10.
 XX Novel Arabidopsis thaliana nucleic acid useful for identifying homologous
 PT or related genes, and to create genetically modified and transgenic
 PT organisms, such as plant cells and plants.
 PS Claim 1; SEQ ID NO 31; 45bp; English.
 XX The invention relates to Arabidopsis thaliana nucleic acid sequences. The
 CC DNA sequences and the polypeptides they encode are useful for identifying
 CC homologous or related genes, for producing compositions that modulate the
 CC expression of the protein, in diagnosis, for studying associated
 CC regions of the protein, for genetic manipulation of cells, preferably
 CC physiological pathways, for screening assays of various plant strains to determine
 CC plant cells, in screening assays of various plant strains to determine
 CC the strains that are capable of withstanding a particular disease or
 CC environmental stress, for enhancing or inhibiting production of
 CC biosynthetic products in plants and to create genetically modified and
 CC transgenic organisms, such as plant cells and plants. Transgenic plants
 CC are useful for introducing or improving disease resistance and stresses
 CC tolerance in plants, screening biologically active agents, such as
 CC fungicides and insecticides, and for elucidating biochemical pathways.
 CC Sequences ABX56649-ABX57647 represent Arabidopsis thaliana
 CC polynucleotides of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
 CC XX
 SQ Sequence 594 BP; 158 A; 116 C; 144 G; 176 T; 0 U; 0 Other;
 Query Match 21.0%; Score 538.8; DB 7; Length 594;
 Best Local Similarity 96.2%; Pred. No. 6e-145;
 Matches 552; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 1971 GTGCACACACAGACTGCTTGTGACAGAGATCGAAGTTCAGAGACTATTCCTTCGCC 2030
 DB 21 GTGCACACACAGACTGCTTGTGACAGAGATCGAAGTTCAGAGACTATTCCTTCGCC 80

QY 2031 AAGTGTATGACGCTGCTGTGTTCCACACAGCAGACAGATTCAGATGCTTCGAT 2090
 DB 81 AAGTGTATGACGCTGCTGTGTTCCACACAGCAGACAGATTCAGATGCTTCGAT 140
 QY 2091 TTGCACTTGTGTGACAGAGTGGGGTAAGACCGGACAGATTCAGTCTGCTTCAGTGC 2150
 DB 141 TCGGACTTGTGTGACAGAGTGGGGTAAGACCGGACAGATTCAGTCTGCTTCAGTGC 200
 QY 2151 GGGTCGAGAGATTCATTCACACAGAGATGATATGAGAGAGAGAGAGAGAGATGAGAG 2210
 DB 201 GGGTCGAGAGATTCATTCACACAGAGATGATATGAGAGAGAGAGAGAGAGATGAGAG 260
 QY 2211 GAGACATGAGATTCATTCACACAGAGATGATATGAGAGAGAGAGAGAGAGATGAGAG 2270
 DB 261 GAGACATGAGATTCATTCACACAGAGATGATATGAGAGAGAGAGAGAGAGATGAGAG 320
 QY 2271 CGAGT 2330
 DB 321 CGAGT 380
 QY 2331 TTTTGTTCCT 2390
 DB 381 TTTTGTTCCT 440
 QY 2391 TATTGAACCCCTGCTTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTAT 2450
 DB 441 TATTGAACCCCTGCTTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTAT 500
 QY 2451 GATCCACTTTTACCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTT 2510
 DB 501 GATCCACTTTTACCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTT 560
 QY 2511 CTCTGTGATTTGATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2544
 DB 561 CTCTGTGATTTGATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 594
 RESULT 12
 ADD18749
 ID ADD18749 standard; DNA; 3256 BP.
 XX
 AC ADD18749;
 DT 15-JAN-2004 (first entry)
 XX
 DE Human disease related protein DNA sequence SegID180.
 XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnerability; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing; gene; ds.
 XX
 OS Homo sapiens.
 XX WO2003018621-A2.
 XX 06-MAR-2003.
 XX 23-AUG-2001; 2001GB-00020558.
 XX 05-OCT-2001; 2001GB-00024037.
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 PA Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 PI WPI; 2003-290046/28.
 DR P-PDB; ADD18748.

XX New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.

XX Claim 27; SEQ ID NO 180; 424bp; English.

XX This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiretioclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.

XX Sequence 3256 BP; 828 A; 761 C; 832 G; 834 T; 0 U; 1 Other;

Query Match 13.9%; Score 358.2; DB 9; Length 3256;

Best Local Similarity 52.4%; Pred. No. 2.6e-82; Indels 27; Gaps 7;

Matches 964; Conservative 0; Mismatches 848;

386 GCTTGTGCTGTGTGTCAGCAAGAGCTTATGCTTATGAGCTATGTTGACCG 445
535 GCTGTGACAGCTGCGGACAGAGTGGCTGATGGCTGTATGAGGCTATTTACCGAG 594
446 CTGATGTGACGCGGACCTCACTTCTGATGATGACATGATTTTGAAGACAGATTTTC 505
595 TACAGCATCTGTGCTGCCAGATTTTGTGACCAATTTGATTTTCAATGACAGAG 654
506 AGAAGCACTTATGAAACTGTCAAGTCTATGCTTATGAGGCTATTTCAATTTTC 565
655 CCGCGGACCTCAATGAGAACCTTCATGAACTCTTAAATGAAATGATTTCCCATGTC 714
566 AATGAGATGATGCTTATGACACCGGAGAGCCCC-----ATATCAGGATTTCTTGGT 619
715 AACCAAAATGATGCTGTTGTCCCGGAGTGGCCCAACAGTACCTCGAGGGGTTATT 774
620 ATTCTGAGATTAACGATAGCTTAGCTGCTTACTGCGCTGGAATCTGAACTGATCTT 679
775 AGGTTAAGATTAATATAGTACCTGCTGCGGCTGCGTGGAAATGAAACTGATCTC 834
680 CTGATTTCTTGAAGCATGTTGAAGTCTTTACACAGGCTTCCAGAGTACTTAACTCA 739
835 TTGATTTGTTCTTCAATGATGAGAGGCTTTTGAACGCCCCCAGGTTCAAGATGACA 894
740 AAGTGTATCAACTTTTGTAAAGAAACATCAAGATGATTAATTTCCGCGACAA 799
895 AAGCTTATGATTAATTTATCCCGAGATCAGAGCTG---TACATTTGGAACCAAG 951
800 TCAAGATTAGAGAGAGGGGTATGATGCAAAAGTCAAAAGCTGCACTCACTTAT 859
952 TTAGAGTGGAGATGGGTGATGAGAGCCAAAGTAAAGACGCTCTGGGCTTTGCA 1011
860 GCTGGGATTTCTGTCATCAATCAAGGAGTATGCTGAGAACTAGATTAAGTCTTC 919
1012 GGTGGCACTTCTGTTGTTATTTGCAATGAAACCCAAAGGTGCTGGGACGTCATC 1071
920 AGAGACTACGATGTGAACTTTGTTCAATCAAGATGCTGTTTATGGGCTCCGATACA 979
1072 ACAGACATGTGAGGGGAGAGAAAGTGT---ACCTTTCTTTCAAAATTAAGCTGCA 1128
980 GATTCTAATGCTGTGACATGAGAGTGTGCGAGAGGAAAGTCCAGAAAGCTTACAGGC 1039
1129 GGGCTTACTGTTGAGCAGCGAGAAATGCGCGATCTGAGAGAAAGATTTGGCCACC 1188

QY 1040 TTATCTTGGAGACAGAGAAAAAATTCGTGTTATATGCGCATGCTTGAAGCAAT 1099
DB 1189 TTGGAATCTGAGCAGAGGACAGAAATATTCATATCTGCTATCTTTGACGACACG 1248
QY 1100 GTTACTACATCAAAAGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1159
DB 1249 CGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1305
QY 1160 GAAAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1219
DB 1306 GCAAGCTCTCTGCTGAAAGCTTTAAGCTCTTCAATCAATTAAGACGCTGCGCATC 1365
QY 1220 TCAGTCTGTAAGCTAGCTGATAT---GGAGATCCAAATGCGCGTGTAAAGAAACA 1276
DB 1366 GGTCTGCAAGATGAGAGCGCTCCACAGACAGCGTGGAGCGTGTTCGCGCGCAC 1425
QY 1277 GAGGTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1336
DB 1426 CGAATGCGCAAAACTTGAACCTGGAACAGTGAAGTGTCCCAATTTGAGTTCTGCTG 1485
QY 1337 GTTTTGAATCCGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1396
DB 1486 ATCTTGAATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1545
QY 1397 AATGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1456
DB 1546 AATGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
QY 1457 GTGATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1516
DB 1606 CTGACCCAGAGGCTCTCTCAATCCATGATGATGATGATGATGATGATGATGATGAT 1665
QY 1517 AGAAGAGATTCCTGATTTGCTTAACTTGAAGCTTATGATGATGATGATGATGATGAT 1576
DB 1666 AGAAGAGATTCCTGATTTGCTTAACTTGAAGCTTATGATGATGATGATGATGATGAT 1725
QY 1577 GGAAGAGAGATTCCTGATTTGCTTAACTTGAAGCTTATGATGATGATGATGATGATGAT 1633
DB 1726 GGTCTCTTCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1785
QY 1634 CATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1693
DB 1786 CACAGGAGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1845
QY 1694 CGATGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1753
DB 1846 AGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1905
QY 1754 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1813
DB 1906 TTATTCACCGGATCTGCTCAAGACACATTAATTTGACACAGATCAATGATGCTGAGA 1965
QY 1814 AGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1867
DB 1966 GTGACAGGATTAATAATCTGACAGGCCCCAAATTTGCTCTCATGCTTCAACCCCC 2025
QY 1868 CCAAGACAGGCTCATTTCAACCATGATGATGATGATGATGATGATGATGATGATGATGAT 1927
DB 2026 TCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2085
QY 1928 GAAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1987
DB 2086 GACACGTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2145
QY 1988 ATTGTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2047
DB 2146 ATGCTTCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2205
QY 2048 GTTCTTCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2107
DB 2206 GTGTTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2265
QY 2108 GTGGGGGTAAGCAGGGCAGAGATTCATGCTGATGCTCAAGTGGGGTGAAGATTAATT 2167

Db 2266 GTGGGAAATGATGATCGAGATCCAGCCCGGAGACAGTAGACTTGAGGACTGCTT 2325
 QY 2168 ACACAGCATGATATAGAGGAAAAGACAAGTTGTC 2206
 Db 2326 ACTACTAAGTGCTGCTGCGAGGAGGACCACTGCTGCT 2364

RESULT 13
 ABN99076/c
 ID ABN99076 standard; DNA; 792 BP.
 AC ABN99076;
 AC 01-AUG-2002 (first entry)
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 844.
 DE Arabidopsis thaliana, plant; insecticide; fungicide; transgenic; stress;
 KM disease; crop; thale cress; tolerance factor; insect; pathogen;
 KM nutrition; ds.
 OS Arabidopsis thaliana.
 XX
 XX US2002023281-A1.
 PN 21-FEB-2002.
 PD 26-JAN-2001; 2001US-00770445.
 PF 27-JAN-2000; 2000US-0178472P.
 PR
 XX
 XX (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAM/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEN A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICK/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX
 PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 DR WPI: 2002-403163/43.
 XX
 XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,
 PT producing compositions that modulate the expression or function of its
 PT encoded protein, and mapping functional regions of protein.
 PS Claim 1, SEQ ID NO 844; 49bp + Sequence Listing; English.
 XX
 XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
 CC comprising a sequence capable of hybridizing under stringent conditions
 CC to a sequence selected from any one of 999 sequences (ABN99233-ABN99231),
 CC given in the specification or its fragment. A polypeptide (II) encoded by
 CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
 CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
 CC useful for screening a candidate agent for its biological effect. (I) is
 CC useful in identifying homologous or related genes, in producing

CC compositions that modulate the expression or function of its encoded
 CC protein, mapping functional regions of the protein and in studying
 CC associated physiological pathways. (I) is also useful for the genetic
 CC manipulation of cells, particularly plant cells. (II) is also useful in
 CC screening assays of various plant strains to determine the strains that
 CC are best capable of withstanding a particular disease or environmental
 CC stress. (III) and (IV) are useful for screening of biologically active
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
 CC pathways. The screened agents are useful in improved methods of treating
 CC crops to prevent or treat disease. (II) are also useful in screening
 CC programs to identify agents that mimic or enhance the action of tolerance
 CC factors. Such agents are useful in improved methods of treating crops to
 CC enhance their tolerance to environmental stress. (I) is also useful for
 CC enhancing or inhibiting production of a biosynthetic product in a plant.
 CC (III) is useful for identifying other mediators that may induce
 CC expression of proteins of interest, for establishing the extent to which
 CC any specific insect and/or pathogen is responsible for damage to a
 CC particular plant, for identifying other mediators that enhance or induce
 CC tolerance to environmental stress, for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial, or medicinal value and
 CC for identifying productions of nutritional, commercial or medicinal
 CC value. (IV) is useful in the study of genetic function and regulation,
 CC for alteration of the cellular metabolism and for screening compounds
 CC that may affect the biological function of the gene or gene products.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docid=99909770445
 XX
 XX Sequence 792 BP; 238 A; 167 C; 138 G; 249 T; 0 U; 0 Other;
 SQ

Query Match 13.5%; Score 346.4; DB 6; Length 792;
 Best Local Similarity 83.0%; Pred. No. 3,2e-89;
 Matches 395; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1776 AGAATGCTGCTTAAGACCTATTGCTGTCAGAGCAATGAGTCACTTGTATG 1835
 Db 792 AGAATGCTTTCGATGATCTTATTATGTTCTGCAACCAAGGCTACCTTTGATG 733
 QY 1836 GTGACCAAGGGCAAGTAACTGAACATACCAAGACCGGTCAATTCAACCATGAGT 1895
 Db 732 GTGGGCCAAGAGCAAGTGCAAACTGAATATTCGGAAACAAATCTTCCACACGAGT 673
 QY 1896 ACTGTGCCAAGCTTTCGCTTGAAGTTGAAGACGTTTATGCTGATGATGATGACA 1955
 Db 672 ACAGTTCAGAGCGCTGACCGTTGAATTTGAAGACGTTATGCTGATGATGATGACA 613
 QY 1956 TTCAACGACATGAGAGTGACACACAGACTGCAATTGTCAGAGGATCAAGATTTCAG 2015
 Db 612 TTCAACCAATGAGAGTGACACACAGCTGATGATGATGAGAGATGATGATGATGAG 553
 QY 2016 AGCTATTCCTTCCGCAAGTGAATGCGCTGCTGCTTCCACACGCAAGCAAGATTCT 2075
 Db 552 AAATATTCCTTCCGCAAGTGAATGCGCTGCTGCTTCCACACGCAAGCAAGATTCT 493
 QY 2076 CAGATGCTTCCGCAATGGAATGCTGTCAGAGAGTGCGGGTGAAGACCGGCGAGATTCATG 2135
 Db 492 CTGATGCTTTTAAAGTTGCGACTTGTGCTGAGTGGAATGAGCAAGACGATTCATG 433
 QY 2136 CTGCTGTCAGAGTGGGGTCCAGAGATTTACTTACACAGATGATATATGAGAGAAAG 2195
 Db 432 CCGGTGTCAGAGTGGAGTTGAGAGATTTATGACAAAGATGATATATGAGAGAAAGG 373
 QY 2196 GACAAAGTTGTGAGAGAGCAATGGAATGTTTACACCAATCAGAGATTCATC 2251
 Db 372 GACAAAGTTGTGAGAGAGCAATGGAATGTTTACACCAATCAGAGATTCATC 317

RESULT 14
 ABX62288
 ID ABX62288 standard; DNA; 418 BP.
 XX
 XX ABX62288;
 AC
 XX

DT 25-FEB-2003 (first entry)
 XX Arabidopsis thaliana expressed sequence related polynucleotide #403.
 DE
 XX Transgenic plant; plant; genetically modified cell; environmental stress;
 KM ribozyme creation; disease resistance; stress tolerance;
 KM fungicide screening; insecticide screening; gene; ds.
 XX Arabidopsis thaliana.
 OS
 XX US2002040490-A1.
 XX
 PD 04-APR-2002.
 XX
 PF 26-JAN-2001; 2001US-00770423.
 XX
 PR 27-JAN-2000; 2000US-0178512P.
 XX
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HMT/) HAMILTON C M.
 PA (PRC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICK/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX
 PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX
 DR WPI; 2003-110411/10.
 XX
 PT Novel Arabidopsis thaliana nucleic acid useful for identifying homologous
 PT or related genes, and to create genetically modified and transgenic
 PT organisms, such as plant cells and plants.
 XX
 PS Claim 1; SEQ ID NO 403; 43bp; English.
 XX
 CC The invention describes an Arabidopsis thaliana nucleic acid (I). The
 CC polypeptide (II) encoded by (I), transgenic plant (III) or genetically
 CC modified cell (IV) are useful for screening a candidate agent for its
 CC biological effect, by combining the candidate agent with (II), (III) or
 CC (IV), and determining the effect of the candidate agent on (II), (III) or
 CC (IV). (I) is useful for identifying homologous or related genes, for
 CC producing compositions that modulate the expression or function of its
 CC encoded protein, for mapping functional regions of the protein, in
 CC diagnosis, for studying associated physiological pathways, for genetic
 CC manipulation of cells, preferably plant cells, in screening assays of
 CC various plant strains to determine the strains that are capable of
 CC withstanding a particular disease or environmental stress, for enhancing
 CC or inhibiting production of biosynthetic product in a plant, for
 CC producing polypeptides, as probes for the detection of mRNA in biological
 CC samples, to generate additional copies of (I), to generate ribozymes or
 CC oligonucleotides, as single stranded DNA probes or as triple-strand
 CC forming oligonucleotides, and to create genetically modified and
 CC transgenic organisms, such as plant cells and plants. (II) or (III) is
 CC useful for introducing or improving disease resistance and stress
 CC tolerance in plants, screening biological active agents, e.g.,
 CC fungicides, insecticides, etc., and for elucidating biochemical pathways,
 CC (III) is useful as crops for their enhanced disease resistance, enhanced

CC traits of interest, for screening programs, as crops which exhibit
 CC enhanced tolerance to environmental stress, or to produce a factor. This
 CC sequence represents a nucleic acid that may correspond to naturally
 CC occurring Arabidopsis thaliana expressed sequences. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docid=99909770423
 XX
 XX Sequence 418 BP; 121 A; 84 C; 103 G; 110 T; 0 U; 0 Other;
 XX
 XX Query Match 12.5%; Score 320.4; DB 7; Length 418;
 XX Best Local Similarity 85.4%; Pred. No. 7.6e-82;
 XX Matches 357; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
 XX
 QY 842 GGAGTCATGACAGCTTATGCTGGAGATTCCTGTCATCATPACAGTGGATTTACGTAG 901
 DB 1 GCTGTTAATGACGCTTATGCTGGAGATTCCTGTCATCATPACAGTGGATTTACGTAG 60
 QY 902 AACATGATPAAAGTCTTCAGAGACTACGTTGGAACCTTTGTTCAATCAAGATGCTTC 961
 DB 61 AATATGATPAAAGTCTTCAGAGACTACGTTGTTGTTACCTTCATCAAGATGCTTCAT 120
 QY 962 TTATGGGCTCCGATACAGATTTCAATGCTGTCATCAAGATGCTGGAGGAAAGT 1021
 DB 121 TTATGGGCTCCGATACAGATTTCAATGCTGTCATCAAGATGCTGGAGGAAAGC 180
 QY 1022 TCCAGAAAGCTTCAAGGCTTATCTTCCGAGACAGAAAMAAATTCGCTTGATATTGCC 1081
 DB 181 TCAAGAAAGCTTCAAGGCTTATCTTCCGAGACAGAAAMAAATTCGCTTGATATTGCC 240
 QY 1082 GATGCGCTTGAAGCAATGTTACTACATCAAGCTGGAATGATGATGATGATGATG 1141
 DB 241 AATGCGCTTGAAGCAATGTTACTACATCAAGCTGGAATGATGATGATGATGATG 300
 QY 1142 GCACAAGAGGCTGGGTTGGAAGATGATGATGATGATGATGATGATGATGATGATG 1201
 DB 301 GCACAAGAGGCTGGGTTGGAAGATGATGATGATGATGATGATGATGATGATGATG 360
 QY 1202 ATCTGAGGCTTGCAGCTTCACTTCTAGCTGATATGAGAAATCCCAATGGGCC 1259
 DB 361 ATCTGAGGCTTGCAGCTTCACTTCTAGCTGATATGAGAAATCCCAATGGGCC 418
 XX
 XX RESULT 15
 XX ID AAC78003 standard; cDNA; 2507 BP.
 XX
 XX AAC78003;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human cancer associated gene sequence SEQ ID NO:397.
 XX
 XX Human; cancer associated gene; cancer antigen; detection; cancer;
 XX diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
 XX antidiabetic; antiaesthetic; antithematic; antithetical; antiviral;
 XX antidiagnostic; antidiagnostic; antidiagnostic; antidiagnostic;
 XX dermatological; neuroprotective; thrombolytic; coagulant; noctropic;
 XX vasotropic; antiproliferative; antineoplastic; gene therapy; inflammation;
 XX immune disorder; haematopoietic cell disorder; autoimmune disorder;
 XX allergic reaction; graft versus host disease; organ rejection;
 XX haemostatic; thrombolytic; cardiovascular disorder; infection;
 XX neurological disease; drug screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN NC0200055350-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000MC-US005882.
 XX
 PR 12-MAR-1999; 99US-0124270P.

Thu Mar 11 07:51:06 2004

us-10-026-767-2.rng

Page 22

Db 1553 GAAGGACCCACGTGGTC 1568

Search completed: March 10, 2004, 11:20:28
Job time : 889.231 secs

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OM nucleic - nucleic search, using SW model

Run on: March 10, 2004, 10:29:50 ; Search time 180.077 Seconds

(without alignments)
7923.149 Million cell updates/sec

Title: US-10-026-767-2

Perfect score: 2571
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued Patents, NA.*
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3: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1156.8	45.0	2417	1 US-07-953-695A-1	Sequence 1, Appli
2	1156.8	45.0	2417	1 US-08-267-258-1	Sequence 1, Appli
3	182.2	7.1	1281	4 US-09-543-681A-1122	Sequence 1122, Ap
4	169.6	6.6	1470	4 US-09-635-587-1	Sequence 1, Appli
5	137.2	5.3	1830121	4 US-09-643-990A-1	Sequence 1, Appli
6	137.2	5.2	276	4 US-09-313-294A-1035	Sequence 1035, Ap
7	132.6	4.8	1254	4 US-09-724-623-44	Sequence 44, Appli
8	124	4.8	261	4 US-09-313-294A-1616	Sequence 1616, Ap
9	122.4	4.8	28171	4 US-08-961-527-22	Sequence 22, Appli
10	122.4	4.7	1278	4 US-09-328-352-3804	Sequence 3804, Ap
11	115.8	4.5	291	4 US-09-313-294A-4491	Sequence 4491, Ap
12	98.6	3.8	294	4 US-09-313-294A-6792	Sequence 6792, Ap
13	95	3.7	462	4 US-09-107-532A-2515	Sequence 2515, Ap
14	93.2	3.6	256	4 US-09-313-294A-3665	Sequence 3665, Ap
15	91	3.5	1059	4 US-09-489-039A-5838	Sequence 5838, Ap
16	87.4	3.4	1289	4 US-09-252-991A-5600	Sequence 5600, Ap
17	87.4	3.4	1611	4 US-09-252-991A-5605	Sequence 5605, Ap
18	87.4	3.4	218	4 US-09-107-532A-1786	Sequence 1786, Ap
19	71	2.8	294	4 US-09-103-840A-2	Sequence 523, App
20	69.6	2.7	4403765	3 US-09-103-840A-2	Sequence 1, Appli
21	68.8	2.7	4411529	3 US-09-103-840A-2	Sequence 2, Appli
22	68.8	2.2	1164	4 US-09-543-681A-889	Sequence 889, App
23	55.4	2.0	1480	4 US-09-134-000C-1373	Sequence 1373, Ap
24	51.4	1.9	1289	4 US-09-673-395A-139	Sequence 139, App
25	49.8	1.9	852	4 US-09-134-000C-1372	Sequence 1372, Ap
26	49.6	1.9	852	4 US-09-134-000C-1372	Sequence 1372, Ap
27	49.6	1.9	852	4 US-09-134-000C-1372	Sequence 1372, Ap

28	47.6	1.9	1149	4 US-09-328-352-355	Sequence 355, App
29	47.4	1.8	1125	2 US-08-709-874A-25	Sequence 25, Appli
30	47.4	1.8	1125	3 US-09-104-382-25	Sequence 25, Appli
31	47.4	1.8	1125	4 US-09-833-555-25	Sequence 25, Appli
32	45	1.8	405	4 US-09-252-991A-5562	Sequence 5562, Ap
33	41.2	1.6	7218	4 US-08-232-463-14	Sequence 14, Appli
34	40.4	1.6	1119	4 US-09-107-532A-2997	Sequence 2997, Ap
35	40.2	1.6	3111	4 US-09-543-681A-3564	Sequence 3564, Ap
36	40.2	1.6	1131	4 US-10-204-708-28	Sequence 28, Appli
37	40	1.6	732	4 US-09-489-039A-5895	Sequence 5895, Ap
38	39.6	1.5	732	3 US-08-998-416-1036	Sequence 1036, Ap
39	39.2	1.5	7218	1 US-08-232-463-14	Sequence 14, Appli
40	38.8	1.5	433	4 US-08-976-259-116	Sequence 116, App
41	38.8	1.5	663	3 US-08-998-416-191	Sequence 191, App
42	38.8	1.5	854	3 US-08-998-416-534	Sequence 534, App
43	38.8	1.5	860	3 US-08-998-416-287	Sequence 287, App
44	38.4	1.5	399	4 US-09-621-976-8976	Sequence 8976, Ap
45	38	1.5	1419	1 US-08-242-098-39	Sequence 39, Appli

ALIGNMENTS

RESULT 1
US-07-953-695A-1
Sequence 1, Application US/07953695A
Patent No. 5344923
GENERAL INFORMATION:
APPLICANT: VERMA, D. et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding For Bifunctional Enzymes For Prol
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kremlas, Foster, and Millard
STREET: 7632 State Ridge Blvd.
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43068
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/953,695A
FILING DATE: 19920929
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foster, Frank H.
REGISTRATION NUMBER: 24,560
REFERENCE/DOCKET NUMBER: URF 2-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 575-2100
TELEFAX: (614) 575-2149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2417 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: Sequence encodes Pyrroline-5-carboxylate synthetase, a bifunctional
FRAGMENT TYPE: N-terminus: N-MESAYDPS--C-terminus: --RRGRGN-C
FRAGMENT TYPE: Internal Fragment: --VDAREMAV--
ORIGINAL SOURCE:
ORGANISM: Vigna acatiffolia
STRAIN: Motbean
DEVELOPMENTAL STAGE: Root nodules
IMMEDIATE SOURCE:

LIBRARY: CDNA expression library
 CLONE: CDNA clone
 PUBLICATION INFORMATION:
 AUTHORS: Chien-An A. Hu, Ashton J. Delaney and Dosh Pal S. Verma
 TITLE: A bifunctional enzyme (delta1-pyridine-5-carboxylate synthetase) catalyz
 JOURNAL: Proceeding of the National Academy of Science USA
 VOLUME: 89
 ISSUE: October
 PAGES: 9354-9358
 DATE: OCT-1992
 RELEVANT RESIDUES IN SEQ ID NO: 1: FROM position 37 to position 2049 GenBank M
 US-07-953-695A-1

Query Match 45.0%; Score 1156.8; DB 1; Length 2417;
 Best Local Similarity 72.7%; Pred. No. 0;
 Matches 1562; Conservative 0; Mismatches 582; Indels 6; Gaps 5;

113 GAGCTAGATCGTTCACGCTTTTCCAGAGACGTCMAAGTATCGTCTTAAGTTGGG 172
 46 GCGGTGATCTTCTCCGGGTTTCATAGAGACGTGAGCTGTATCATCAAGTTGGC 105
 173 ACAGCAGTTGTTACTGAAAAAGTGAAGATTGGCTTTGCTTTAGAGACATGTGT 232
 106 ACCCGGTGTCTACCTCCGAAAGAGAGATTAGCGGTGAAAGATTGGAGCTCTGTGC 165
 233 GAACAGCTGGGAATTAACCTGGATGATTTGAGGTGATTTGGGTGATCTGGTGG 292
 166 GAGCAGATTAAAGCACTCACTCTCTCGATAGCAATTAATCTCTCTCTGCCCC 225
 293 GTTGGTCTTGGCAGCAAGGCTTCGTTATGACAAATTAAGTCAATAGACCTTGGCAT 352
 226 GTCCGATTGAGCAAGGCTACGTTCCGTAATTAATCAACAGCAGCTTCCGCGAC 285
 353 CTGAGAGCCTCAGACTGAACTTGATGGAGGCTTGTGCTGTGTTGAGCAAGAGT 412
 286 CTTCAGAAACCCCACTGAACTGACGCGAAGGCTGCGCGCTTGGACAGAAAGT 345
 413 CTTAATGCTTAATGAGACTATGTTGACCAAGCTTATGATGACGAGCTCACTTCTG 472
 346 CTCAATGCTCTCAAGATAGCTGTCTCACTGATGATGATGATGATGATGATGAT 405
 473 GTGATGACATTAATTTAGAGACAGAGATTCAAGAGCACTTAATAGCACTGACAG 532
 406 GTGACGATTAAGATTTGAGATAGAGATTTCAAGAGCACTTACTGACCTGAGAG 465
 533 TCTATGCTTGAATTTAGGGTTATTCATTTTCAATAGATATGCTATTAAGACCCGA 592
 466 TGGCTGTGGCGGAGAGGTTATCCGGTGTTCATAGAGACATGCGTTAGTACAGG 525
 593 AGAGCCCATATCAGGATTTCTTGTGATTTTTCGGATTAAGATAGCTTACTGCTCTA 652
 526 AAGGCTCCCTTCAAGAGATTTCTTGTGATTTTTCGGATTAAGATAGCTTACTGCTCTA 585
 653 CTGGCTTGAAGTGAAGTGTATCTTCTGATCTTCTGACGATTTGAAGGCTTTTAC 712
 586 TTAGCTTGAAGTTAAAGCCGATCTCTTGTGTTGTTGATGATGATGATGATGATGAT 645
 713 ACAGCCCTTCAAGTATCTTCACTCAAGTTGATCCACTTTTGTGTTAAAGAAAAAT 772
 646 AGTGCCCTTCAAGGAGCCCTTCAATCAAGCTTATTTATCATTTAAACAAAGAAAAAT 705
 773 CAAGATGATTAATCACTTGGGAGCAAAATCAAGATTAGGAGAGAGGGGTATAGTCAAAA 832
 706 CAGATGAAATTTCTTTTGGGAGCAAGCTTGAAGTGAAGAGGCGAATGAGCTGCCAAA 765
 833 GTCAAGTGTGACATGATGACGCTTATGCTGGATTTCTCTCATCATCAAGTGGGTAT 892
 766 GTAAAGCTGCGGTTCAATGACGCTGAGCTGCAATTCCTGTGTTATTAACAGAGGTTT 825
 893 TCAGCTGAGACATGATTAAGTCTCAGAGACATGACGTTGAGCACTTGTTCATCAA 952
 826 GCACTGAGAAATCATTAATTTCTTCCAGAGCAAGCTATAGAGAACTCTCTTCCATAAA 885

953 GATGCTGTTTATGGGCTCCGATCAAGATTTATGCTGTGATGAGCAAGTTGCTGCG 1012
 886 GATGACATAGTGGGCTCAAGTAAAGAGTTGATCAAGTGAAGGCTGTTGACGC- 944
 1013 AGGAAATGTCAGAAAGCTTCAGGCTTATCTTCGAGAGACAGGAAA-AAAAATTCGT 1071
 945 AGGAAATGTCAGAAAGCTTCAGGCTTATCTTCAGAGAGAGGAAAACAAATTTTACT 1004
 1072 TGAATTTGCCAGTCCCTTGAAGCAATTTGTTACTATCAATCAAGCTGAGATGAGTTAGA 1131
 1005 TAAATAGCTATGCTCCGAGAGCAAAATGAAATATATCAAGATTGAAATGAGCTGA 1064
 1132 TGTAGCTTCTGACAGAGGCTGGGTGGAAGATCATGATGATGCTGCTTATGATGAC 1191
 1065 TGTATCTCTGACAGAGAGAGATATGAAAAATCTTGTGCTTGAAGCTTAA 1124
 1192 ACTTGAAAGATCTGAGCTTGCAGCTTCAAGTTGATGATGATGATGATGATGATGAT 1251
 1125 ACTTGAAAGATCTGAGCTTGCAGCTTCAAGTTGATGATGATGATGATGATGATGAT 1184
 1252 AATGGCGGTGTTTAAAGAAAACAGAGTGGCAGATGATGATGATGATGATGATGATGAT 1311
 1185 AATTGATGAGATTAATTAAGCTACGAGCTTCAAGTGGCTAATTTTGAAGAAATCATC 1244
 1312 ATCAACATTAAGCGCTACTTCTGATTTGTTTGAATCCGACCTGATGATGATGATGAT 1371
 1245 ATCTCTTGGAGAGCTCTTATTTGTTTGAATGATGATGATGATGATGATGATGATGAT 1304
 1372 AGCTTCACTTGCATCCGTTATGGAATGATGATGATGATGATGATGATGATGATGATGAT 1431
 1305 AGCTTCACTTGCATCCGTTATGGAATGATGATGATGATGATGATGATGATGATGATGAT 1364
 1432 GCGATCAATGCTATCTTACCAAGAGTATCATGATGATGATGATGATGATGATGATGAT 1491
 1365 GCGATCAATGCTATCTTACCAAGAGTATCATGATGATGATGATGATGATGATGATGAT 1424
 1492 TAAATCTTGAAGCTTGTGATTTCAAGAGAGATGATGATGATGATGATGATGATGATGAT 1551
 1435 AAAATCTTGAAGCTTGTGATTTCAAGAGAGATGATGATGATGATGATGATGATGATGAT 1464
 1552 GGTATGATGCTTGTGATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1611
 1485 TGTATGATGCTGATTTCCAGAGGAGATGATGATGATGATGATGATGATGATGATGAT 1544
 1612 TACAAAAATCCCTGTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1671
 1545 AACTAAAAATCCCTGTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1604
 1672 TGTATGATGCTTGTGATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1731
 1605 TGTATGATGCTGATTTCCAGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1664
 1732 CTGATGATGCTGATTTCCAGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1791
 1665 CTGATGATGCTGATTTCCAGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1724
 1792 TGAAGCTATTTTGTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1851
 1725 GAGATCATTTCTTGAATCTTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1784
 1852 TAAATGATGCTGATTTCCAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
 1785 TTTCTGTTAAATTTTCCAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1844
 1912 CACTGTTGAAGTTGAGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1971
 1845 CACCGCCGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1904
 1972 TGCACACACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2031
 1905 TGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1964
 2032 AGTGAATAGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2091

Db 1965 AGTAGACAGTCTGCTGTTTTCACATGACACCAAGTTCAAGTAGGGGACAGATT 2024
QY 2092 TG-GACTTGTGACAGAGTGGGGGTAAAGCAGGCGAGATCCATGCTGCTGCTCAGTGC 2150
Db 2025 TGAGACTAGGCGGAGAGGTTGAATTAAGTCAAGCAGGATTCATGCTCAGAGGTGAGTGC 2084
QY 2151 GGGTCGAAGATTACTACACAGAGATGATGATTAAGAGAGAAAGCAAGTTGTCAGC 2210
Db 2085 AGTT--GAGATTTCTTACACAAAGATGATTAAGAG--AAGGACAAAGTGTGATG 2141
QY 2211 GAGCAATGGAATTTTAAACCCATCAGACATTCCTCCATCAAGCTTAA 2260
Db 2142 GTGATAGAGGCGTTGCTACACCCACAAAGACCTTGCAATTTAATTAA 2191

RESULT 2
US-08-267-259-1
Sequence 1, Application US/08267259
Patent No. 5639950
GENERAL INFORMATION:
APPLICANT: VERMA, D. et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding For Bifunctional Enzymes For Pro-
Patent No. 5639950
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Kumbhakar, Foster, and Willard
STREET: 7632 State Ridge Blvd.
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43068
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,259
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/953,695
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Foster, Frank H.
REGISTRATION NUMBER: 24,560
REFERENCE/DOCKET NUMBER: DRF 2-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 575-2149
TELEFAX: (614) 575-2149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: Sequence encodes Pyrroline-5-carboxylate synthetase, a bifunctional
Patent No. 5639950
FRAGMENT TYPE: N-terminus: N-MEVAVDP--
FRAGMENT TYPE: C-terminus: --RRGRN-C
FRAGMENT TYPE: Internal Fragment: --VDAREMAV--
ORIGINAL SOURCE:
ORGANISM: *Vigna aconitifolia*
STRAIN: Mothbean
DEVELOPMENTAL STAGE: Root nodules
IMMEDIATE SOURCE:
LIBRARY: cDNA expression library
CLONE: cDNA clone
PUBLICATION INFORMATION:
AUTHORS: Chien-An A. Hu, Ashton J. Delaney and Dosh Pal S. Verma
TITLE: A bifunctional enzyme (deltaal-pyrroline-5-carboxylate synthetase) catalyz

JOURNAL: Proceeding of the National Academy of Science USA
VOLUME: 89
ISSUE: October
PAGES: 9354-9358
DATE: OCT-1992
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM position 37 to position 2049 GenBank N
US-08-267-259-1
Query Match 45.0%; Score 1156.8; DB 1; Length 2417;
Best local similarity 72.7%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 582; Indels 6; Gaps 5;

QY 113 GAGTAGATCGTTACAGTCTTTTCCAGAGACCTCAACCTATCCGTCCTTAAGTGGG 172
Db 46 GCGGTGATCCCTTCGCGGGGTTCATGAGAGACGTGAAGCGTGTATCATCAAGTTGGC 105
QY 173 ACAGCAGTTGTTACGTGAAGAAGTGAAGATTTGGCTCTTGCTTTAGAGCAGTGT 232
Db 106 ACCGCGGTGTCATCTCGGAGAGAGAGAGATTTACGGTTGGAAGATTGGAGCTCTGTC 165
QY 223 GAAACGCTTGGGAATTAACCTCGATGATTTAGAGTATTTGCTGTATCTGTCG 292
Db 166 GAGCAGATTAAAGCACTCACTCTCGGATACACATTAATACCTCTCTGCGCC 225
QY 223 GTTGTCTTGGCAGGCAAGGCTTGTATGACATTAAGCAATGACAGCTTGGCAG 352
Db 226 GTGGTATTTGACCGCCAGAGCTTACGTTCCGTAAATTAACACAGAGCTTGGCAG 285
QY 353 CTTCAAGACCTCAGACTGAACCTTGATGGAAGCTTGTCTGTGTTGCAAGACAG 412
Db 286 CTTCAAGAACCCCACTGAACCTGACGAGCGGAGGCTGCGCGCTTGGCAAGACAG 345
QY 413 CTTATGCTTCTATGACATGATTTGACAGCTGATGAGCGGAGCTCACTTCTG 472
Db 346 CTTATGCTTCTTACGATACGCTGTCTCACTGATGATGATGATGATGATGATGAT 405
QY 473 GTGAATGACAGTATTTAGAGACAGAGATTTCAGAGAACTTAATGAAGTGTCAAG 532
Db 406 GTGACGATTAACGATTTTCAGATTAAGATTTTCAGAGAGAGCTTACGACCTGTGA 465
QY 533 TCTATGCTTGTATGAGGCTTATTCATTTTCAATGAGATGATGATGATGATGATG 592
Db 466 TCGCTGTGGCGCTGAAGGTATTCGCTGTTCATGAGAGAGAGGCTTATGATGAG 525
QY 593 AGAGCCCATATCAGAGATTTCTGTGATTTTCTGGAATTAAGATGATGATGATG 652
Db 526 AAGGCTCCCTATGAGATTTCTGTGATTTTCTGGAATTAAGATGATGATGATG 585
QY 653 CTGGCGTTGGAAGTGAAGCTGATTTCTGATCTCTGACGATGATGATGATGATG 712
Db 586 TTAGCTTTGAGTGAAGAGCGGATCTCTGTTGTTGATGATGATGATGATGATG 645
QY 713 ACAGCCCTCCAGAGATCTTACTCAAGTGTATCCACCTTTGTTAAAGAAACAT 772
Db 646 AATGGCCCTCCAGAGATCCCTATTCATTAAGCTTATTAATTAATTAATTAATTA 705
QY 773 CAAGATGATTAATTTGAGGAGCAATCAAGATTAAGGAGAGGAGGATGATGATG 832
Db 706 GGAATGAATTAATTTGAGGAGCAATCAAGATTAAGGAGAGGAGGATGATGATG 765
QY 833 GTCAAGCTGAGTCAATGAGCTTATGCTGGGATTTCTGTATCATCAAGTGGAT 892
Db 766 GTTAAAGCTGCGTTCAAGAGCTTATGCTGGGATTTCTGTATCATCAAGTGGAT 825
QY 893 TGAAGTGAACATTAAGTGAAGTCTCAAGAGATGATGATGATGATGATGATG 952
Db 826 GCACTGAGATTAATTAATTTCTCAAGAGCAAGATTAAGGAGATCTCTCAATTA 885
QY 953 GATGCTGTTTATGAGGCTCCGATCAAGATTTATGCTGATGATGATGATGATG 1012
Db 886 GATGCAATGATGAGGCTCAAGATTAAGGATTAAGGATGATGATGATGATGATG 944
QY 1013 AAGGAAAGTTCCAGAAAGCTTATGCTTATGATGATGATGATGATGATGATG 1071

Db 945 AGGGAATGTCGAGAGGCTCCAGCCGTTATCTTCAGGAGAAAGAAACAAATTTACT 1004
 Qy 1072 TGAATTCGCGTGCCTTGAAGCAATGTTACTACATCAAGCTGAGATGAGTGA 1131
 Db 1005 TBAATAGCTGATGCCCTCGAAGCAATGAAAAATATATCGATGTAATGAACTGA 1064
 Qy 1132 TGTAGCTTCTGCAAGAGGCTGGTGAAGAGTCATGAGTGGCTGCTTATGATGAC 1191
 Db 1065 TGTACTGCTGCACAGAGAGCAGATATGAAAAATCCCTGGTGGCTAGGCTTTAAA 1124
 Qy 1192 ACCGGAAAGATCTGAGGCTTCAGCTTCAGTTGTAAGCTGATATGAAAGATCC 1251
 Db 1125 ACCTGGAAAGATGCAAGCTTCGCAACATGCAATCATTTGCCATATGAAAGATCC 1184
 Qy 1252 AATCGCGCTGTTTAAAGAAAAAGAGTGGCAGATGCTTGTCTTGAAGAAACCTC 1311
 Db 1185 AATTGGTGGATTAATAACGTAACGAGCTTCAGATGGCTTAATTTAGAAAAAGATC 1244
 Qy 1312 ATCAGCATAGGCGTACTTGTGATTTTGAATCCGCACTGATGACTTGTACAGAT 1371
 Db 1245 ATCTCCTTGGAGGCTCCTTATTTGTTGAGTCACTGCTGATGCTTTTACAGAT 1304
 Qy 1372 ACCTTCACTGCGCATCCGTAAGTGAATGATCTTCTGCTGAAGGCTGGAAGAGCCG 1431
 Db 1305 ACCTTCACTGCGCATCCGTAAGTGAATGATCTTCTGCTGAAGGCTGGAAGAGCCG 1364
 Qy 1432 GCGATCAATGCTATCTTACACAGAGTATCATGATGCAATTCAGAGACTGTTGGGG 1491
 Db 1365 GCGATCAATGCTATCTTACACAGAGTATCATGATGCAATTCAGAGACTGTTGGGG 1424
 Qy 1492 TAACTCATTTGACTTGTGATCTTCAAGAGAGAGATTCCTGATTTGCTTAACTTGA 1551
 Db 1425 AAACTTANAGACTTGTGATCTTCAAGAGAGAGATTCCTGATTTGCTTAACTTGA 1484
 Qy 1552 CGTTATGATCTTGTGATCTTCAAGAGAGAGATTCCTGATTTGCTTAACTTGA 1611
 Db 1485 TGTATTTGATCTTGTGATCTTCAAGAGAGAGATTCCTGATTTGCTTAACTTGA 1544
 Qy 1612 TACAAAAATCCCTGCTGATGCTCATGCTGATGATGCTCATGATGCTGATGCTG 1671
 Db 1545 AACTTAAATCTTCTGTTTATGCTCATGCTGATGATGCTCATGATGCTGATGCTG 1604
 Qy 1672 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1731
 Db 1605 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1664
 Qy 1732 CTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1791
 Db 1665 CTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1724
 Qy 1792 TGAAGTATTTTGTCTGTCAGAGCATGAGTCACTTGTATGATGATGATGATG 1851
 Db 1725 GAGATATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1784
 Qy 1852 TAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1911
 Db 1785 TTTCTGTTATATATCTTCAAGAGATGATGATGATGATGATGATGATGATGATG 1844
 Qy 1912 CACTGTTGAAGTGTGAGAGAGCTTTATGATGATGATGATGATGATGATGATGATG 1971
 Db 1845 CACCGCGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1904
 Qy 1972 TGAACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2031
 Db 1905 TGAACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1964
 Qy 2032 AGTGAATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2091
 Db 1965 AGTGAATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2024
 Qy 2092 TG-GACTTGTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2150

Db 2025 TGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2084
 Qy 2151 GAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2210
 Db 2085 AGTT--GAGATTTGTTAAACACAGATGATGATGATGATGATGATGATGATGATG 2141
 Qy 2211 GAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2260
 Db 2142 GTGATGAGGCGTGTCTTACAGCCCAAGAGCTTGCATTTATTTTAA 2191

RESULT 3
 US-09-543-681A-1122
 ; Sequence 1122, Application US/09543681A
 ; Patent No. 6605768
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; PRIORITY FILING DATE: 1999-04-09
 ; PRIORITY FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 1122
 ; LENGTH: 1281
 ; TYPE: DNA
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-1122

Query Match 7.1%; Score 182.2; DB 4; Length 1281;
 Best Local Similarity 48.5%; Pred. No. 1.1e-46;
 Matches 588; Conservative 0; Mismatches 598; Indels 27; Gaps 2;

Qy 996 ACATGCACTTGTGCTGAGAGAGAGTTCAGAAAGCTTCAGGCTTATCTTGAAGACA 1055
 Db 38 AAATGGAAAAGGCGCGAGAGAGCTTCTGGCATAGCTAGCTATCAACGAAACAA 97
 Qy 1056 GGAATAAATTCCTGCTGATATTCGAGATGCCCTTGAAGCAATGTTACTACATCAAG 1115
 Db 98 AAATAGGACAGCTGTAGTCATGCTGATTTATTAAGACAGAGAGCATTAATTCCTG 157
 Qy 1116 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1175
 Db 158 CTCTATGATAAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 217
 Qy 1176 CTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1235
 Db 218 ATGTTTATTAATCAATCAAGAAAGCTTAAAGAGATGCTGATGATGTTCCCAAGTT 277
 Qy 1236 CTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1295
 Db 278 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 337
 Qy 1296 TCTTAAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1355
 Db 338 GTTAAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 397
 Qy 1356 ATGCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1415
 Db 398 ATGCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 457
 Qy 1416 GTGAAAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1473
 Db 458 GCGAAAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 517
 Qy 1474 -----TCAAGAGCTGTTGGGGTAACTCAATTGATGATGATGATGATGATGATG 1526
 Db 518 AAACATGCTGATTTCTGCGCGCTGATTAAGCTATGATGATGATGATGATGATGATG 577
 Qy 1527 TTCCTGATTTGCTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1586


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Db      578 TCGCAAAATGCTAAATATGATGATATATGATATGCTTATTCCTGAGGTGTCAG 637
Qy      1587 AGCTTGTACTGAGATATAAATATCTACAAATATCCCTGTAGATCATGTGATGAA 1646
Db      638 GATTATATAGTATATGCTGGAACATCAATATTCCTGTATCAAGGGGGGATTTGAT 697
Qy      1647 TCTGTATATATATGTCGCAAGGCTTGTGATACGATATGCGCAAGCGCATGTTCTG 1706
Db      698 TTTGTACACCTTTGTTGACGAAGGCTGATTTAGACCAAGCATTAATGTTATATTA 757
Qy      1707 ATCAAGATTTGACATTCAGCAGCTCTATATGCGATGGAACCTTCTGTGATTAAG 1766
Db      758 ATCTTAAAGTTCAGCTCCAGAGCATATATTCGTTAAGACGATATGTCATGAG 817
Qy      1767 ATCTAAGCAGATGCTGTGCTTAAAT-----GAGCTTATTTTCTC 1808
Db      818 CTATTCGGGAGATTTCTTCCCTCAATTAAGATGCGATGCGACACAAAGGTTACTT 877
Qy      1809 TGCAGAGCAATGAGTCACTTTGTATGTGACCAAGGCGAATGATGATGAACTATC 1868
Db      878 TGATGCGCATCAAGCGCTATATCTGATGATGAAAAGGAGCTGCGACGTCGTGATG 937
Qy      1869 CAGAGCAGCGTCATTCACCATGAGTACTGTGCGAAGGCTTGCACCTGTTGAAGTTGAG 1928
Db      938 TGACAGAGCAGATATTTGATGATGATGCTATCACTGATCTGATGTTGAAGTCGTTA 1997
Qy      1929 AAGACGTTATGCTGTATATGATCATTCACCGAATGAGAGTGCACACAGACTGCA 1988
Db      998 ATGATTTAAGCGGGGCAATTTGCTCATTTGCGCAATATGTTACCGGCACTGATGCTA 1057
Qy      1989 TTGTGACAGAGATCAAGAGTTGCGAGCTATTTCTTCCCAAGTGAATAGCGCTGTG 2048
Db      1058 TTTTAAGCAATATATCAATGATGATGATGCTGTTTACCGCAAGTGAATGCTGCGGG 1117
Qy      2049 TGTTCACACAGCGCAGACAGAAATTTCTGATGATTTCCGATTTGACCTGTGTCAGAG 2108
Db      1118 TATATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1177
Qy      2109 TGGGGGTAAGCAGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2168
Db      1178 TAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1237
Qy      2169 CAAAGAGATGAT 2181
Db      1238 CCTATAAATGAT 1250

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US-09-635-587-1

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; Sequence 1, Application US/09635587
; Patent No. 6423307
; GENERAL INFORMATION:
; APPLICANT: HITACHI, LTD
; TITLE OF INVENTION: Promoter of Arabidopsis thaliana for 71-pyrroline-
; TITLE OF INVENTION: carboxylate-synthetase
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/635,587
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: promoter
; DATABASE ACCESSION NUMBER: AB022784
; DATABASE ENTRY DATE: 1999-01-28
US-09-635-587-1

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Query Match 6.6%; Score 169.6; DB 4; Length 1470;
 Best Local Similarity 97.7%; Pred. No. 1.1e-42;
 Matches 172; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 CTGATATTTATTTTCTTACTTAAATACAGCGGTGCTTCACTGAGTCCGACTGATTAAC 60
Db      1278 CTGATATTTATTTTCTTACTTAAATACAGCGGTGCTTCACTGAGTCCGACTGATTAAC 1337
Qy      61 TCGTTCCTCTCTGCTGTGTGTGTTTGTGATGACGACGACGATATGAGAGGCTAGA 120
Db      1338 TCGTTCCTCTCTGCTGTGTGTGTTTGTGATGACGACGACGATATGAGAGGCTAGA 1397
Qy      121 TCGTTCAGTGTCTTTTCCGAGAGAGCTCAACGATATGCTTAAAGTTGGACAG 176
Db      1398 TCGTTCAGTGTCTTTTCCGAGAGAGCTCAACGATATGCTTAAAGTTGGAG 1453

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US-09-557-884-1/c

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; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS V6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

```

Query Match 5.3%; Score 137.2; DB 4; Length 1830121;
 Best Local Similarity 47.3%; Pred. No. 2.5e-30;
 Matches 544; Conservative 0; Mismatches 573; Indels 33; Gaps 3;

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Qy      1075 TATGCGGATGCGCTGAGAGCAATGTTACTACATCAAGCTGAGATGATTAGATGT 1134
Db      1312924 TATGCGAAGAAATCTGACAAACAAGACACCGCTTATCTTAGCGGAAACCAAGATAT 1312865
Qy      1135 AGCTTCTGCAACAAGGCTGAGTTGGAAGATCAATGCTGCTTATGATGACAC 1194
Db      1312864 TGAACCTGCCAAACAAATGATATGATGATGCTTATGATGCTTACTGCTACACA 1312805
Qy      1195 TGAAGAATCTGAGCGCTGAGCTTCAAGTCTGATGATGATGATGATGATGATGAT 1254
Db      1312804 AGAAGCTTTACAGAGCATTGTATGATGATGATGATGATGATGATGATGATGAT 1312745

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QY 1255 CGGCCGTGTTTAAAGAAACAGAGGTGGCAGATGCTTCTTTAGAGAACTCATC 1314
 DB 1312744 GGGGAAATCATAGCGCGGTACATGGATAGGGAATTAAATGAAAGCGGTACGAC 1312685
 QY 1315 ACCATTAGCGCTACTTCTGATGTTTGAATCCGACCTGATGCACTTGTACAGATAGC 1374
 DB 1312684 TCCGCTAGCGGTATGTTAGCAATTATGAGAGCTGCGCAATGTAACATGATGAGG 1312625
 QY 1375 TTCACTTCCCATCCGTAGTGGAAATGCTTCTGCTGAAGAGGTGGAAAGAGGCGCGG 1434
 DB 1312624 AAGCTTTGCTTTAAAGGGGTAAGCAGTATTTAGCGCGTGTAAAGAAACACAGTT 1312565
 QY 1435 ATCAATGCTATCTTACACAAAGTATGATGATGCAATTCAGAGACTGTGGGGGTAA 1494
 DB 1312564 TTCTAACAAAGATTTTAAATGCAAGTTGTGCAAAATCCTTTAGAGCAAGAGCTTACCAA 1312505
 QY 1495 ACTCATTTGAGACTTGTGACTTC-----AAGAGAGAGATTCCTGATTTGCTTAAAGT 1545
 DB 1312504 ATTTGCGGTGCAAGCATACCATCCGATCCAAACCGTGAACCTGTTATGCAATTTAAACT 1312445
 QY 1546 TGATGACGTTATGATCTGTTGATGATCCCAAGAGAAAGCAAGCTTGTACTCAGATAA 1605
 DB 1312444 GATGCGCTATGATGATGATGATTTATCTGCTGCTGCTTCCGCTTATCATGATTTGTGTA 1312385
 QY 1606 AATTACTACAAATCCCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1665
 DB 1312384 ACATCATTCGATATTCCTGTTATGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1312325
 QY 1666 CAAAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1725
 DB 1312324 AAAAGGTGCGATCAAAATTAAGCGATTTTGTATGATTAACCCCAAAACCCCAACGTC 1312265
 QY 1726 AGCAGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1785
 DB 1312264 AAGCAGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312205
 QY 1786 GCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1845
 DB 1312204 AACTA---AAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1312148
 QY 1846 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1884
 DB 1312147 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312088
 QY 1885 CAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1944
 DB 1312087 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312028
 QY 1945 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2004
 DB 1312027 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1311968
 QY 2005 CGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2064
 DB 1311967 AAGCTTACCGGTCAATTTATCAATCAATGATGATGATGATGATGATGATGATGATGAT 1311908
 QY 2065 CACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2124
 DB 1311907 CACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1311848
 QY 2125 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2184
 DB 1311847 AAAATCTTACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1311788
 QY 2185 GAGAGGAAA 2194
 DB 1311787 TGAAGGCGAA 1311778

RESULT 6
 US-09-643-990A-1/c
 ; Sequence 1, Application US/09643990A

Patent No. 6528289
 GENERAL INFORMATION:
 APPLICANT: Robert D. Fleischmann
 Mark D. Adams
 Owen White
 Hamilton O. Smith
 J. Craig Venter
 TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments thereof, and Uses therefor
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville,
 STATE: MD
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3 1/2 inch diskette
 COMPUTER: Dell Pentium
 OPERATING SYSTEM: MS DOS v6.22
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/643,990A
 FILING DATE: 23-Aug-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/487,429
 FILING DATE: 1995-06-07
 APPLICATION NUMBER: 08/426,787
 FILING DATE: 1995-04-21
 ATTORNEY/AGENT INFORMATION:
 NAME: Kenley K. Hoover
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: FBI86P1C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-610-5790
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1830121 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-643-990A-1
 Query Match 5.3%; Score 137.2; DB 4; Length 1830121;
 Best Local Similarity 47.3%; Pred. No. 2.5e-30;
 Matches 544; Conservative 0; Mismatches 573; Indels 33; Gaps 3;
 QY 1075 TATGCGCATGCCCTTGAAGCAATGTTACTACAAATCAAGCTGAGAAATGATTGATG 1134
 DB 1312924 TATGCGCAACAACCTCGAACAAGCAACCGCTTATCTTACCGCAAAACGAAAGAT 1312865
 QY 1135 AGCTTGTGCAACAAGCGGTGGTGGAGAGTCAATGATGATGATGATGATGATGATGATGAT 1194
 DB 1312864 TGAATCTGCAACAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1312805
 QY 1195 TGAAGAATCTGAGCCTTGACGCTTCAATGATGATGATGATGATGATGATGATGATGAT 1254
 DB 1312804 AGAAGCTTACCAAGCATGCTAATGATGATGATGATGATGATGATGATGATGATGAT 1312745
 QY 1255 CGCGCGTGTTTAAAGAAACAGAGGTGGCAGATGCTTGTGCTTAGAGAAAGACTCATC 1314
 DB 1312744 GGGGAAATCATAGCGCGGTACATGGATAGGGAATTAAATGAAAGCGGTACGAC 1312685
 QY 1315 ACCATTAGCGCTACTTCTGATGTTTGAATCCGACCTGATGCACTTGTACAGATAGC 1374
 DB 1312684 TCCGCTAGCGGTATGTTAGCAATTATGAGAGCTGCGCAATGTAACATGATGAGG 1312625
 QY 1375 TTCACTTCCCATCCGTAGTGGAAATGCTTCTGCTGAAGAGGTGGAAAGAGGCGCGG 1434

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Db 1312624 AGCTTTGGCTTAAACGGGTAATGAGTATTTTACCGGGTGTAAAGAACCACTT 1312565
Qy 1435 ATCAAAATGCTATCTTACACAAAGGTGATCACTGATGCAATTCAGAGACTGTGGGGGTAA 1494
Db 1312564 TTCTAACAGATTTTATGAGAGTTGTGCAAAATGCTTAGAGCAAGCGCTTACCAA 1312505
Qy 1495 ACTGATTGACCTTGACTTC-----AGAGAGAGATTTCTGATTTGCTTAAGT 1545
Db 1312504 ATTGGGGTGCAGCAAGCAATTCAGATCAAAACCGTGAACCTGTAGCAATTTAAACT 1312445
Qy 1546 TGATGACGTTATGATCTTGTGTGATCCCAAGAGAACCAAGCTGTGATCTAGATTA 1605
Db 1312444 GATTCGCTATGATGATATGATTTATTCCTGTGTGTGGGTTTACAGAAATGATGA 1312385
Qy 1606 AATATCTACAAAATCCCTGTGTGTAGTATGATGATGCAATCTGATGATTAATGCA 1665
Db 1312384 ACAACATTCGACTATTCCTGTATTTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGT 1312325
Qy 1666 CAGGCTGTGATACGGAATATGCAAGCGCATGATTTCTGATGCAAAAGTTGACTATCC 1725
Db 1312324 AAAAATGCGGATCAAAATTAAGCGATTTTGTATGATTAAGCAAAACCAAGCTCC 1312265
Qy 1726 AGCAAGCTGTATGCAATGCAAGAAACCTTCTGTGCAAAAGATCTAGACAGATGCTGT 1785
Db 1312264 AAGCACTGTATACCAATTTGAAACATTTGATTTCAATTTGATTTGATTTGATTTT 1312205
Qy 1786 GCTTATGACCTATTTTGTCTGTGCAAGCAATGAGTCACTTGTATGATGCAAG 1845
Db 1312204 ACCTA--AAGTGTCTTACCTTCCGCTTAAACGTAATTAATTAATTAATTAATTA 1312148
Qy 1846 GCGAAGTATGATATCTGAACATACCAAG-----AAGCAGCGTAT 1884
Db 1312144 CGCACTTATATATTTGAAACAGCGGGTGCAGATGCTGCAAGATGACAGAAAGAAAT 1312088
Qy 1885 CAACATGATGATCTGTGCAAGCTTGCATGTTGAAGTTGTGAAGACGTTTATGATGCT 1944
Db 1312087 GCGAAGATGAGGATGATGATTTGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1312028
Qy 1945 TATGATCATCATTCACCGACATGAGAGTGCACACAGACTGATGTCACAGAGATCA 2004
Db 1312027 TATGACATATTCGCCAATATGATGACCAATTCGAAAGATTTTAACTTCCACACA 1311968
Qy 2005 CGAAGTTGACAGATTTCTTGTGCAAGTGTAGCGCTGTGTGTGTGTGTGTGTGTGTGT 2064
Db 1311967 AAGCTTACCGCTTCAATTTATCAATCAAGTTGATGCGGACCGCTTATGATTAATCA 1311908
Qy 2065 CACAAGATTCAGATGATGATTTCCGATTTGCACTTGTGCAAGAGTGTGGGTTAGCAAG 2124
Db 1311907 CACAGCTTATGATGATGCGGACCAATTTGATTTAGGCGCAAGATTTGCCGTAGTACCA 1311848
Qy 2125 CAGATCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2184
Db 1311847 AAACCTTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1311788
Qy 2185 GAGAGGAAA 2194
Db 1311787 TGAAGGCGAA 1311778

```

RESULT 7
US-09-313-294A-1035
Sequence 1035, Application US/09313294A

Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: P-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program
SEQ ID NO 1035
LENGTH: 276
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 7005027.H1
NAME/KEY: unsure
LOCATION: 6, 28, 56, 118, 144, 182, 237, 245, 256
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-1035

Query Match
Best Local Similarity 70.3%; Pred. No. 1,5e-31;
Matches 185; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

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Qy 582 TTACACCCGAGAGCCCATATCAGATTTCTGTGATTTTCTGGGATTAAGATAGT 641
Db 1 TCAGCCTAGAAAGGCTCCATATGAGGTTTCACTGTATTTCTGGATTAATGAAAGTT 60
Qy 642 TAGTGCTTACTGCGGTGGAAGCTGAACTGATCTTCTGATTTCTGAGGATGTTG 701
Db 61 TAGCTGTCTTTTGGCTATTTGAACTTAAAGCAATCTCTGTTCTACTAAGTAGAG 120
Qy 702 AAGGCTTTACAGAGCCCTTCA-AGTATCTTAACTCAAGTTGATCAACTTTGTT 760
Db 121 ATGCTATACAGGGGTCCACANAGCAACCGGATCAAGATCAATTCATCTTCAATC 180
Qy 761 AAAGAAAACATCAAGATGATTTACATTTGGGAGCAAAATAGAGAGAGGGGGT 820
Db 181 AAGATTAACATTCAGTGAATTAATTTGGGATTAATGATGATGATGATGATGATGATG 240
Qy 821 ATGACTGCAAAAGTCAAGCTGC 843
Db 241 ATGAGCTAAAGTGMAGGCTGC 263

```

RESULT 8

US-09-724-623-44
Sequence 44, Application US/09724623

Patent No. 6476209
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Lubbers, Mark W
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: chem, and methods for using them.
FILE REFERENCE: 1048U1
CURRENT APPLICATION NUMBER: US/09/724,623
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 1254
TYPE: DNA
ORGANISM: Lactobacillus rhamnosus
US-09-724-623-44

Query Match
Best Local Similarity 4.8%; Score 124; DB 4; Length 1254;
Best Local Similarity 46.9%; Pred. No. 2.2e-28;
Matches 545; Conservative 0; Mismatches 590; Indels 27; Gaps 4;

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Qy 1068 TGCTGATATGCGCATCCCTTGAAGCAATGTTACTACATCAATCAAGCTGAGATGAT 1127
Db 101 TGTGGCATGTGATAGGCTCTTGAAGCATCTGAAGCAATTTTGGAGCTATATATG 160
Qy 1128 TAGATGATCTTCTGACACAGAGGCTGTGGAAGACTCAATGTGCTGCTTATGTA 1187
Db 161 AAGATCTAAAGCGGCA-----GCAAGCTTCCGGCTTAACTTCAAGGATGATGATG 214
Qy 1188 TGACACCTGAAAGATTCGAGCCTTGAGCTTCACTTCACTGATGATGATGAG 1247

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Db 215 TGACAGCCGAGCGATTCCTGACATGCGAGAGGGGTTCCGCAAGTTGCCGCTTACTTG 274
 Qy 1248 ATCCAAATCGCGCGTGTAAAGAAAAAGAGGTGGAGATGCTTGTCTTAAGAGAGA 1307
 Db 275 ATCCAAACCGCCAGAGGATGAGCGCTGGGTGAATCAAGAGAGCTGAATATATGCCAAA 334
 Qy 1308 CCTATACACCAATTTGGGGTACTTCTGATTTGTTTGAATCCGACCTGATGACCTTGTAC 1367
 Db 335 AACGGGTACTTTAGGGGTGGTGGGATGATTTAGGGGCCCGGCAATATGATACCGTTG 394
 Qy 1368 AGATAGCTTCACTTCCATCCGATGAGAAATGCTTCTTCTGTAAGGGTGAAGAGAG 1427
 Db 395 ATGCTGCTGGGTAACTTTTAAAGTGGCAATGGGTCATTTCTCCGGGGGTAAAGAG 454
 Qy 1428 CCGCGGATCAATATCTTAAAGAGATGATCACTGATGATGCAATCCGAGACTGTTG 1487
 Db 455 CGGTGACAGCAATTTGGCTTGGCGACCTTTTACAGGCTGATGACGCAAGAT 514
 Qy 1488 GGGGTAACCTGATGACTTGTGA-----CTTCAAGAGAGAGATTCCTGATTG 1538
 Db 515 TGCCAAAAGACGGATTCATTAATACAGGACCGAGCCGAGAGAGATGCGAATCAAGTGA 574
 Qy 1539 TTAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1598
 Db 575 TGCACTGGAATGCTACATGATGCTGATTCGCGGTGGTGGCGAGGTTGATTAAG 634
 Qy 1599 AGATTAATAATACATAAAATCCCTGTGATGATGATGATGATGATGATGATGATGAT 1658
 Db 635 CAGTGTGGAACAGGCTTACCTTACCTGATGATGATGATGATGATGATGATGATGATG 694
 Qy 1659 ATGTGACAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1718
 Db 695 ATGTGATGCTTATGCGAGAGCCGAGATGATGATGATGATGATGATGATGATGATG 754
 Qy 1719 ACTATCAGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1778
 Db 755 AGCGGCGCTGTGTTTGGCATGAGCGCCAGAACTTTATTCACGCTGATGATG---CA 811
 Qy 1779 ATGTGCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1838
 Db 812 ACGGCGAGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 871
 Qy 1839 GACCAAGGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1889
 Db 872 ATGAACGGGCGCGGCAATGTCGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 931
 Qy 1890 ATGAGTACTTGCAGAGCTTGCATGCTGTAAGTTGTAAGAGCTTTATGCTATAG 1949
 Db 932 CCGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 991
 Qy 1950 ATCAGATTCAGCAGATGAGAGTGCACACAGCTGATGATGATGATGATGATGATGATG 2009
 Db 992 CGCATATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1051
 Qy 2010 TTGAGAGCTTATCCTTGGCAGAGTGAAGCGTGTGTTTCCACAGCCAGCAGCA 2069
 Db 1052 ATAGTCAGCAATCTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1111
 Qy 2070 GATTCTCAGATGTTTCCGATTTGCACTTGTGTAAGAGTGGGGGTGAAGCAAGGCGAGGA 2129
 Db 1112 GGTTCACAGAGCGGCTTCAAGTTGCTTTCGCGCAGAGATGATGATGATGATGATGATG 1171
 Qy 2130 TCCATGCTCGTGTGCTGAGTGGGTCGAAGATTAATTAACAAGATGATGATGATGATGATG 2189
 Db 1172 TACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1231
 Qy 2190 GAAAGAGCAAGTTGTCAGCG 2211
 Db 1232 GTAAAGGACAGGTACGCGAAG 1253

RESULT 9
 US-09-313-294A-1616

; Sequence 1616, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Laljudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313, 294A
 ; NUMBER OF SEQ ID NOS: 1999-05-14
 ; CURRENT FILING DATE: 1999-05-14
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1616
 ; LENGTH: 261
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700551225H1
 ; NAME/KEY: unsure
 ; LOCATION: 243
 ; OTHER INFORMATION: a, t, c, g, or other
 ; US-09-313-294A-1616
 ;
 Query Match 4.8%; Score 122.6; DB 4; Length 261;
 Best Local Similarity 69.3%; Pred. No. 2.1e-28;
 Matches 167; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
 ;
 Qy 1921 AGTGTATGAACCGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
 Db 1 ATTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 Qy 1981 AGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
 Db 61 AGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
 Qy 2041 CGCTCTGTGTTCCACAGCGCAGCAGCAAGTTCTCAAGTGTTCGATTTGATGATGATG 2100
 Db 121 TGCCCTGTGTTTCAATATGAGCAGCAAGGTTTGTATGAGACGCTTTTGGGCTAGG 180
 Qy 2101 TGCAGAGTGGGGTGAAGCAGGCGAGATCATGCTGATGATGATGATGATGATGATGATG 2160
 Db 181 TGTGAGTGGCATTAAGTATAGAGCGCATACATGCGCGGAGCTGTGTGATGATGATG 240
 Qy 2161 A 2161
 Db 241 A 241
 ;
 RESULT 10
 US-08-961-527-22
 ; Sequence 22, Application US/08961527
 ; Patent No. 6420135
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunesh
 ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 391
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/961,527
 ; FILING DATE:
 ; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: P3340P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28171 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-961-527-22

Query Match 4.8%; Score 122.4; DB 4; Length 28171;
 Best Local Similarity 47.0%; Pred. No. 6,36-27;
 Matches 578; Conservative 0; Mismatches 616; Indels 36; Gaps 5;

1049 GAAGACGAGAAAAAATTCCTGATATATGCGCATGCGCTTGAGCAAAATGTTACTACA 1108
 5903 GAAGTGAACAAACCAAGCTTGTGCTAGCCATGCTGATCACTTAGTGGCTGCTACTGAGGA 5962
 1109 ATCAAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1168
 5963 ATTATGAGGCTATATGCGCTGATATGCGAGCGCTTAAGGGAATCTCAATGATG--- 6019
 1169 ATGTGCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1228
 6020 ATGTGATGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6079
 1229 AAGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1288
 6080 GAATGCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6139
 1289 GGTCTTGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1348
 6140 GGTGTTGTTATCAAAAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6199
 1349 CGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1408
 6200 GGTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6259
 1409 CTGAAGGCTGGAAGGAGGCGCGGATCA---ATCTATCTTACACAGATGATCACT 1465
 6260 CTTCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6319
 1466 GATGCAATTCAGAGACTGTTGGGGGTAACTCACTTGAAGCTTGG-----ACTTCAAGA 1519
 6320 GGTCTGAGAGAGACTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 6379
 1520 GAAGAGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
 6380 GAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6439
 1580 AGCAACAGCTTGTACTCAGATTAATAAATCTACAAAATCCCTGTGCTAGTCTGCT 1639
 6440 GGAAGCTGCTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6499
 1640 GATGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1699
 6500 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6559
 1700 GTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1759
 6560 ATCAACATGCTTAACCAAGTGTCTCTGTTGTTATGATGATGATGATGATGATGATGATGAT 6619
 1760 CATAGAG-----TCTAGAGAGATGCTGTGCTTATGATGATGATGATGATGATGATGATGAT 1798
 6620 CATAG 6679

1799 ATTTTGTCT---CTGACAGCATGAGTCACTTTGATGATGATGATGATGATGATGATGATGAT 1855
 6680 AAGAGAGCTGAGCTGAGCAATTAATTCGCTTATGATGATGATGATGATGATGATGATGATGAT 6739
 1856 ATCTGACATATCAAG 1915
 6740 TCAAGTCAAG 6799
 1916 GTTGAAGTTGAG 1975
 6800 GTTGAAGTTGAG 6859
 1976 CACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2035
 6860 CATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6919
 2036 GATAGCGCTGCTGTGTTCCACAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2095
 6920 GACTCTGACAGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6979
 2096 CTGCTGACAGAGTGGGGTTAAGCAGCGGAGAGATGATGATGATGATGATGATGATGATGATGAT 2155
 6980 CTGCTGTTGAATGGGATTTCTACTAGAAATTCAGCGCGGTGCTCCATGCGCTTG 7039
 2156 GAAGATTAATTAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2215
 7040 AAGAGTTGACAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7099
 2216 AATGATGTTTATCAACCATCAGACATT 2245
 7100 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7129

RESULT 11

US-09-328-352-3804
 ; Sequence 3804; Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 3804
 ; LENGTH: 1278
 ; TYPE: DNA
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-3804

Query Match 4.7%; Score 120; DB 4; Length 1278;
 Best Local Similarity 48.2%; Pred. No. 4,1e-27;
 Matches 472; Conservative 0; Mismatches 490; Indels 18; Gaps 4;

1242 TGAAGATTCATGCGCGCTGTTTAAAGAAACAGAGGTGGCAGATGCTTGTCTTGA 1301
 230 TTGTTGATTCATGAGGAAATTCAGATCTTGATATGCGCCACAGGCAATCAATG 349
 1302 AGAAGACTCATCACTTATGAGCGTACTGATGTTTGTGAATCCGACTGATGAC 1361
 350 GGAAGATGCGTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 409
 1362 TTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1421
 410 CACTTGAAGCTGACATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
 1422 AGAGAGCGCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1481
 470 CAGAGCACTTGAAGTCAATTAAGCAATGCGAGAGCGGTGAACATGCTTAAGATG 529
 1482 CTGTTGGGGGTAACTCATGAGACTTGTGACTTCAA-----GAGAGAGATTCCTG 1552

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Db      530 CTGGTTACCTGACGCTGATGCAAGTGAATTTGAAACTCTTGACCGCTGACGGGTGCTC 589
Qy      1533 ATTGGCTTAAGCTTGAATGAAGCTTATCGATCTTGTATGCCAAGAGAAACAACAGCTTG 1592
Db      590 ACCCTATCTACTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
Qy      1593 TTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1652
Db      650 TTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 709
Qy      1653 ATGTATATGTCGACGAGCTTGTGATACCGATATGCGAAGCGCATAGTTCTGATGCA 1712
Db      710 ATGTGTTTGAAGAGACAAAGCGACTTACAAAAGCGTTACATTTACCTGATGATGCTA 769
Qy      1713 AGTGGACATATCGACAGAGCTTGTATGCGATGAGAAACCTTTCTTGAT -AAGATGTA 1771
Db      770 AAACACATGCTATCGGCGTTTGTATGCAATGAAACCTGCTCGTTGATGAAAAAATTG 829
Qy      1772 GAGCAGATATGCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1830
Db      830 CAGAACTTTCTTACACACATTTGCTGAGCTTTATGCTGAAAAAACAAGTTGATGATGCTG 889
Qy      1831 GTATGTTGACCAAGGCG-----AGTAAGATATCTGAACATACCAAGACAGCGTCA 1883
Db      890 GTTGCCCAAGAAACACGCTGATTTTGAAGAGCTCTGTAACCTGCGACAGAGAGAT 949
Qy      1884 TCACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1943
Db      950 GGTATCCGAAATTTTGAAGACGATTTCTTGACATTTAAAGTGTGACGCTATGATGAA 1009
Qy      1944 CTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2003
Db      1010 CAATTGACCATATCAACAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1069
Qy      2004 AGCAATGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2063
Db      1070 ATACTTGGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1129
Qy      2064 GCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2123
Db      1130 CAACCTGTTTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1189
Qy      2124 GCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2183
Db      1190 ATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1249
Qy      2184 TGAGAGAAAGAGACAGTT 2203
Db      1250 TGTTAGTGAAGCTCAATT 1269

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RESULT 12
US-09-313-294A-4491
; Sequence 4491, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4491
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 70034851SH1

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; NAME/KEY: unsure
; LOCATION: 205
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4491
Query Match
Best Local Similarity 4.5%; Score 115.8; DB 4; Length 291;
Matches 188; Conservative 0; Mismatches 102; Indels 1; Gaps 1;
Qy      712 CACAGGCTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
Db      1 CACGCGTCCACCAAGGAAACCGGATCAAAAGATCATCTTACCTACATTAAGATTAACA 60
Qy      772 TCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 831
Db      61 TTACAGTGAATTAATCTTTGGGATTAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 120
Qy      832 AGTCAAGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 891
Db      121 AGTGAAGCTGCTTTTGTGGCTTGAACAGTGGACACCTGTTGATTAACAAGTGAAT 180
Qy      892 TTGAGCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 950
Db      181 TGCACTTCAGAGCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Qy      951 AAGATGCTGTTTATGAGGCTCCGATCAAGATTTCTATCTGTCATG 1001
Db      241 AGATGCAATCTGTGGAGCCATCAAGAGATGTTAGTCTGTGATGATG 291
RESULT 13
US-09-313-294A-6792
; Sequence 6792, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6792
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700352413H1
US-09-313-294A-6792
Query Match
Best Local Similarity 3.8%; Score 98.6; DB 4; Length 294;
Matches 146; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
Qy      91 GACAGACAGACGATATGAGAGAGCTAATGCTTACAGTCTTTTGCAGAGAGCTCAA 150
Db      67 GNCATGGCCATGGCCATGAGACCGCCGATCTGCGCTGATTTGTAAGAGAGCTCAA 126
Qy      151 ACGATCGTGTAAAGTTGGGACAGAGTGTACTGAAAAAGGTGAAGATGGCTCT 210
Db      127 GCGAATATATTAAGAGTGGGACAGGCTGTGTGATCTGGCATGAATGGCCGATGGCCAT 186
Qy      211 TGGTGTGAGAGCACTGTGTGAACAGCTTGGGAATTAACCTGAGATGATTTAGGT 270
Db      187 GGGAGGCGNCGTTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
Qy      271 GATTTGCTCATCTGTGCGGTTGTGCTTGGCAGAGCAAGGCTTC 317

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Db 247 GATTTCGTAACCTCAGAGAGCTTGTGTGTGGAGGAGAGGCTCC 293

RESULT 14
US-09-107-532A-2515
Sequence 2515, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arlinello, Pamela Denke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 893-5007

TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 2515:

SEQUENCE CHARACTERISTICS:

LENGTH: 462 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...462

SEQUENCE DESCRIPTION: SEQ ID NO: 2515:

US-09-107-532A-2515

Query Match

Best Local Similarity 3.7%; Score 95; DB 4; Length 462;

Matches 170; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

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Db 164 CTGTCAAGTGTGATCTTTGATGAAACAAATGCAATATCAATGCGCATTAATCTA 223

Db 1974 CACACAGACTGATGATGACAGAGGATCAGAAAGTTGAGAGCTATTCCTCGCCAA 2033

Db 224 AACATTCAGAAAGATGATGATAGTATGAGGCTAGTCAACGTTCTTAATGAAG 283

Db 2034 TGAATAGCGCTGCTGTGTTCCACAGCCGACACAGATTCAGATGTTTCCGATTG 2093

Db 284 TGAACGCGCGCTGTATGATGCAATGCTTCACTCGTTTACAGAGGATCGATTTG 343

Qy 2094 GACTTGTGACAGAGTGGGGTAAAGCAGCGGACGATCCATGCTGTGTCAGTCGGGG 2153

Db 344 GTTTTGTGACAGATTTGATCTCTACTCAAAAGTTGATGCGCCGTTGCTCAATGGGCT 403

Qy 2154 TCGAAGATTACTTACCAACGAGATGATTAATGAGAGAAAAGACAAAGTTGTGCA 2208

Db 404 TAAATGATTAATCTTCCACAAATATATCATTTATGCGATGAGCAAAATCCGGCA 458

RESULT 15

US-09-313-294A-3665

Sequence 3665, Application US/09313294A

Patent No. 6476212

GENERAL INFORMATION:

APPLICANT: Ito, Laura Y.

APPLICANT: Ito, Laura Y.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

FILE REFERENCE: PL-0017 US

CURRENT APPLICATION NUMBER: US/09/313,294A

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program

SEQ ID NO 3665

LENGTH: 256

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incycle ID No. 6476212 700612075H1

US-09-313-294A-3665

Query Match

Best Local Similarity 3.6%; Score 93.2; DB 4; Length 256;

Matches 152; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Db 90 AGACGACGACGACGATATATGAGAGGCTAGATCGTTCGCTTTTCCAGACGCTCA 149

Db 7 AGCCCCGCGCGCGGTATGCGCCACCGACAGACCGGATTTTCATGAAGACGCTCA 66

Qy 150 AACGATGCTGTTAAGTTGGGACAGCAATTTTACTGGAAGGGAAGATTGGCTC 209

Db 67 AACGCTATATCAAGGTGGGCACTGCAAGTTGCAAGGCAATGATGGGAGATATCA 126

Qy 210 TTGTCGTTTGAAGACACTGTGTAACAGCTTGGCGAATTAATCGATGATTTGAG 269

Db 127 CAGGAATTTTGGTGTCTTTGTGTAACAGGTGAAGAGATTAATGCTCTAGATACAGG 186

Qy 270 TGAATTTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 329

Db 187 TGAATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246

Qy 330 TAGTCAATAG 339

Db 247 TTGTCAATAG 256

Search completed: March 10, 2004, 12:07:03
Job time : 193.077 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: March 10, 2004, 10:27:40 ; Search time 839.374 Seconds
(without alignments)
11202.698 Million cell updates/sec

Title: US-10-026-767-2

Perfect score: 2571

Sequence: 1 ctcgatacttcttcttacc.....tcagatacttcttcttcc 2571

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues 4842108

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA.*

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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2571	100.0	2571	14 US-10-026-767-2	Sequence 2, Appl1
2	2154	83.8	2154	9 US-09-938-842A-1391	Sequence 1391, Ap
3	2154	83.8	2154	11 US-09-938-842A-1391	Sequence 1391, Ap
4	1669.8	64.9	2181	9 US-09-938-842A-1866	Sequence 1866, Ap
5	1669.8	64.9	2181	11 US-09-938-842A-1866	Sequence 1866, Ap
6	1170.4	45.5	2499	12 US-10-424-599-44242	Sequence 44242, A
7	1085.6	42.2	2549	14 US-10-026-767-1	Sequence 44248, A
8	1053.2	41.0	2708	12 US-10-424-599-44248	Sequence 44248, A
9	1049.2	40.8	2447	12 US-10-425-114-5243	Sequence 5243, Ap
10	1046	40.7	2563	12 US-10-425-114-4280	Sequence 4280, Ap
11	1046	40.7	2563	12 US-10-425-114-32617	Sequence 32617, A
12	1042.2	40.5	2612	12 US-10-425-114-3880	Sequence 3880, Ap
13	953.6	37.1	1952	12 US-10-424-599-44244	Sequence 44244, A
14	947.6	36.9	1708	12 US-10-425-114-8653	Sequence 8653, Ap

16	746	29.0	2214	15 US-10-260-238-466	Sequence 466, Ap
17	572	22.2	1601	12 US-10-425-114-8907	Sequence 8907, Ap
18	515.4	20.0	1345	12 US-10-425-114-24396	Sequence 24396, A
19	494.2	19.2	903	12 US-10-424-599-44403	Sequence 44403, A
20	494.2	18.0	1321	12 US-10-425-114-21021	Sequence 21021, A
21	461.6	18.0	1241	12 US-10-424-599-43856	Sequence 43856, A
22	442	14.9	1218	15 US-10-260-238-33117	Sequence 33117, Ap
23	383.4	14.9	876	12 US-10-424-599-44245	Sequence 44245, A
24	346.4	13.5	752	9 US-09-770-445-844	Sequence 844, Ap
25	342.6	13.3	2907	14 US-10-171-581-114	Sequence 114, Ap
26	292.4	11.4	2507	9 US-09-925-301-397	Sequence 397, Ap
27	291.6	11.3	568	15 US-10-260-238-3278	Sequence 3278, Ap
28	281.6	11.0	576	15 US-10-260-238-5797	Sequence 5797, Ap
29	221.4	8.6	1281	15 US-10-369-493-43699	Sequence 43699, A
30	220.4	8.6	843	12 US-10-424-599-11549	Sequence 11549, A
31	219.4	8.5	541	12 US-10-424-599-93815	Sequence 93815, A
32	211	8.2	1299	15 US-10-369-493-44637	Sequence 44637, A
33	203.6	7.9	1281	15 US-10-369-493-42747	Sequence 42747, A
34	195.8	7.6	570	15 US-10-260-238-4888	Sequence 4888, Ap
35	192.2	7.5	1302	15 US-10-369-493-26502	Sequence 26502, A
36	191.4	7.4	1383	15 US-10-369-493-25789	Sequence 25789, A
37	179	7.0	1251	12 US-10-282-122A-32901	Sequence 32901, A
38	176.4	6.9	1163020	15 US-10-396-221-10	Sequence 10, Appl
39	176.4	6.9	3011208	15 US-10-396-221-2058	Sequence 2058, Ap
40	171.8	6.7	1257	12 US-10-282-122A-15665	Sequence 15665, A
41	165.4	6.4	395	12 US-10-424-599-58022	Sequence 58022, A
42	161.4	6.3	1248	12 US-10-282-122A-24417	Sequence 24417, A
43	158.4	6.2	1233	12 US-10-282-122A-18176	Sequence 18176, A
44	156.4	6.1	7695	9 US-09-070-927A-537	Sequence 537, Ap
45	152	5.9	1251	12 US-10-282-122A-39130	Sequence 39130, A

ALIGNMENTS

RESULT 1
US-10-026-767-2
Sequence 2, Application US/10026767
Publication No. US20030014774A1
GENERAL INFORMATION:
APPLICANT: Hitachi, LTD.
APPLICANT: RIKEN
APPLICANT: Japan International Research Center for Agricultural Science
APPLICANT: Bio-oriented Technology Research Advancement Institute (BRAIN)
TITLE OF INVENTION: Transgenic rice plant and its family with environmental
TITLE OF INVENTION: stress resistant by proline accumulation of high level and its
FILE REFERENCE: NT01P0353
CURRENT APPLICATION NUMBER: US/10/026,767
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 2
LENGTH: 2571
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: 107...2260
AUTHORS: Yoshu Yoshida, Tomohiro Kiyasue, Takeshi Katsagiri, Hiroko
AUTHORS: Yoda, Yoshiaki Mizoguchi, Kazuko Yamaguchi-Shinozaki, Keishiro
AUTHORS: Wada, Yoshimori Harada, Kazuo Shinozaki
TITLE: Correlation between the induction of a gene for 1-
TITLE: pyroline-5-carboxylate synthetase and the accumulation of
TITLE: proline in Arabidopsis thaliana under osmotic stress.
JOURNAL: The Plant Journal
VOLUME: 7
ISSUE: 5
PAGES: 751-760
DATE: 1995-01-20
DATABASE ACCESSION NUMBER: D32138
DATABASE ENTRY DATE: 1994-07-12
US-10-026-767-2

QY 1367 CAGATAGCTTCACTTCCATCCGTAGTGAATGCTCTTCTGCTGAAGGTGGAAGAG 1426
 DB 1261 CAGATAGCTTCACTTCCATCCGTAGTGAATGCTCTTCTGCTGAAGGTGGAAGAG 1320
 QY 1427 GCCCGGCATCAATGCTATCTTACACAAGGTGATCACTGATGCAATTCAGAGACTGT 1486
 DB 1321 GCCCGGCATCAATGCTATCTTACACAAGGTGATCACTGATGCAATTCAGAGACTGT 1380
 QY 1487 GGGGGTAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1546
 DB 1381 GGGGGTAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 QY 1547 GATGAGCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1606
 DB 1441 GATGAGCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 QY 1607 AATGCTACAAAATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1666
 DB 1501 AATGCTACAAAATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 QY 1667 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1726
 DB 1561 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 QY 1727 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1786
 DB 1621 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 QY 1787 CTTATGAGCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1846
 DB 1681 CTTATGAGCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
 QY 1847 GCAATGAGCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1906
 DB 1741 GCAATGAGCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
 QY 1907 GCTTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1966
 DB 1801 GCTTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
 QY 1967 GGGAGTGCACACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2026
 DB 1861 GGGAGTGCACACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
 QY 2027 GCCCAAGTGCACACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2086
 DB 1921 GCCCAAGTGCACACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 QY 2087 GCAATGAGCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2146
 DB 1981 GCAATGAGCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
 QY 2147 GTCGGGCTGCAAGATTAATTCAACAAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2206
 DB 2041 GTCGGGCTGCAAGATTAATTCAACAAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
 QY 2207 GACGAGAGCAATGAGATTTTACACCAATGAGCAATTTCCATCCAGCTTAA 2260
 DB 2101 GACGAGAGCAATGAGATTTTACACCAATGAGCAATTTCCATCCAGCTTAA 2154

RESULT 3

US-09-938-842A-1391
 ; Sequence 1391, Application US/09938842A
 ; Publication No. US20040009476A8
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krepes, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1391
 ; LENGTH: 2154
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1391

Query Match 83.8%; Score 2154; DB 11; Length 2154;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ATGAGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 166
 DB 1 ATGAGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 QY 167 GTTGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 226
 DB 61 GTTGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 227 CTTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 286
 DB 121 CTTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 287 GGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346
 DB 181 GGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 347 GCGGATCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 406
 DB 241 GCGGATCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 407 AGCAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 466
 DB 301 AGCAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 467 CTTTCTGAGATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
 DB 361 CTTTCTGAGATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 527 GTCAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586
 DB 421 GTCAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 587 ACCCGAAGAGCCCATATGAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
 DB 481 ACCCGAAGAGCCCATATGAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 647 GCTCTAGTGGGCTGGAATGGAAGCTGATCTTCTGATTTCTGATCTTCTGAGAGATTTGAAGGT 706
 DB 541 GCTCTAGTGGGCTGGAATGGAAGCTGATCTTCTGATTTCTGATCTTCTGAGAGATTTGAAGGT 600
 QY 707 CTTTACAGAGCCCTTCAAGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGAT 766
 DB 601 CTTTACAGAGCCCTTCAAGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGAT 660
 QY 767 AACATCAAGATGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGAT 826
 DB 661 AACATCAAGATGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGATGATCTTCAAGAT 720
 QY 827 GCAAAAGTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 886
 DB 721 GCAAAAGTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 887 GGTATTCAGCTGAGAGCAATGATTAAGCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 946

Db 781 GGGTATTCAGTGAGAAATAGATTAAGTCTCAGAGAGCACTAGCTGTGAACTTGT 840
 QY 947 CATGAAGTGTCTGTATATGAGGCTCCGATCAAGATTTCTAATGCTGTGCAATGGAATT 1006
 Db 841 CATGAAGTGTCTGTATATGAGGCTCCGATCAAGATTTCTAATGCTGTGCAATGGAATT 900
 QY 1007 GCTCGAGAGGAAAGTTCCAGAAAGCTTCAGGCTTATCTTCGGAAGACAGAAATAAT 1066
 Db 901 GCTCGAGAGGAAAGTTCCAGAAAGCTTCAGGCTTATCTTCGGAAGACAGAAATAAT 960
 QY 1067 CTGCTTATATGCTCCGATGCTTGAAGCAATTTCTAATCAATCAAGCTGGAATGAG 1126
 Db 961 CTGCTTATATGCTCCGATGCTTGAAGCAATTTCTAATCAATCAAGCTGGAATGAG 1020
 QY 1127 TTGATGATGCTTGTGACAAAGAGGCTGGGTGGAAGATCAGTGGCTGCTAGATT 1186
 Db 1021 TTGATGATGCTTGTGACAAAGAGGCTGGGTGGAAGATCAGTGGCTGCTAGATT 1080
 QY 1187 ATGACACCTGGAAGATCTGAGGCTTGCAGCTTCACTGTAAGCTGATGATGAA 1246
 Db 1081 ATGACACCTGGAAGATCTGAGGCTTGCAGCTTCACTGTAAGCTGATGATGAA 1140
 QY 1247 GATCCAAATGCGGCGTGTAAAGAAACAGAGGTGGCAATGCTGTGCTTGAAGAG 1306
 Db 1141 GATCCAAATGCGGCGTGTAAAGAAACAGAGGTGGCAATGCTGTGCTTGAAGAG 1200
 QY 1307 ACCTCATCACCATTAGGCGTACTTCTGATGTTTTTAAATCCGACCTGATGACTGTA 1366
 Db 1201 ACCTCATCACCATTAGGCGTACTTCTGATGTTTTTAAATCCGACCTGATGACTGTA 1260
 QY 1367 CAGATGCTTCACTTGGCATCCGATGCGATGGAATGCTTCTGCTGAAGGTTGAAAGAG 1426
 Db 1261 CAGATGCTTCACTTGGCATCCGATGCGATGGAATGCTTCTGCTGAAGGTTGAAAGAG 1320
 QY 1427 GCCCGGAGATCAAAATGCTATCTTACAAAGAGTATCTGATGCAATTCGAGAGCTGT 1486
 Db 1321 GCCCGGAGATCAAAATGCTATCTTACAAAGAGTATCTGATGCAATTCGAGAGCTGT 1380
 QY 1487 GGGGGTAACTCAATGGAAGCTTGTGACTTCAAGAAAGATTCGATTTGCTTAAGCTT 1546
 Db 1381 GGGGGTAACTCAATGGAAGCTTGTGACTTCAAGAAAGATTCGATTTGCTTAAGCTT 1440
 QY 1547 GATGAGCTTATGATCTTGTGATCCGAAAGAGAGAAACAAGTTGTTCTGAGATTA 1606
 Db 1441 GATGAGCTTATGATCTTGTGATCCGAAAGAGAGAAACAAGTTGTTCTGAGATTA 1500
 QY 1607 AATTAACAATAATCCCTGTGTAGAGTCAATGCTGATGATGATGATGATGATGAT 1666
 Db 1501 AATTAACAATAATCCCTGTGTAGAGTCAATGCTGATGATGATGATGATGATGAT 1560
 QY 1667 AAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726
 Db 1561 AAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1727 GCAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
 Db 1621 GCAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 QY 1787 CTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
 Db 1681 CTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 QY 1847 GCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1906
 Db 1741 GCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 QY 1907 GCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1966
 Db 1801 GCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 QY 1967 GGGAGTGAACACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2026
 Db 1861 GGGAGTGAACACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920

QY 2027 GCCCAAGTGAATGAGCTGCTGTGTTCCAAACCGCAGACAGATTCAGATGATGTT 2086
 Db 1921 GCCCAAGTGAATGAGCTGCTGTGTTCCAAACCGCAGACAGATTCAGATGATGTT 1980
 QY 2087 CGATTTGAGCTTGGTGCAGAGGTGGGAGTAAAGCACGGGACAGATTCAGATGATGTT 2146
 Db 1981 CGATTTGAGCTTGGTGCAGAGGTGGGAGTAAAGCACGGGACAGATTCAGATGATGTT 2040
 QY 2147 GTGGGGTGCAGAGTAACTTACAAAGAGATGATTAATGAGAGGAAAGCAAGTTGTC 2206
 Db 2041 GTGGGGTGCAGAGTAACTTACAAAGAGATGATTAATGAGAGGAAAGCAAGTTGTC 2100
 QY 2207 GACGGAGCAATGGAATGTTTAAACCCATCAGAGATTCCTCCATCCAGCTTAA 2260
 Db 2101 GACGGAGCAATGGAATGTTTAAACCCATCAGAGATTCCTCCATCCAGCTTAA 2154

RESULT 4

US-09-938-842A-1866
 ; Sequence 1866, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: S000-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1866
 ; LENGTH: 2181
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1866

Query Match 64.9%; Score 1669.8; DB 9; Length 2181;
 Best Local Similarity 86.2%; Pred. No. 0;
 Matches 1848; Conservative 0; Mismatches 297; Indels 0; Gaps 0;
 QY 107 ATGAGAGAGCTAAGTCTGTTCAAGCTTTTGGCCAGAGAGCTCAACGATATGCTGTTAAG 166
 Db 1 ATGAGAGAGAGCTAAGTCTGTTCAAGCTTTTGGCCAGAGAGCTCAACGATATGCTGTTAAG 60
 QY 167 GTTGGAGACAGAGTGTCTTACGGAAGAGTGAAGATTGCTCTGTGCTTTAGAGACA 226
 Db 61 GTTGGAGACAGAGTGTCTTACGGAAGAGTGAAGATTGCTCTGTGCTTTAGAGACT 120
 QY 227 CTGTGTAAACGCTTGGCGAATTAACTCGATGATGATTTGAGTGATATGCTGTCACT 286
 Db 121 ATCTGTGAACAGCTTGGCGAAGTTAACTCAGATGATGATTTGAGTGATATGCTGTCACT 180
 QY 287 GGTGCGGTGTGCTTGGCAAGCAAGGCTCTGATTCGACAAATTAAGCATACAGCTT 346
 Db 181 GGTGCGGTGTGCTTGGCAAGCAAGGCTCTGATTCGACAAATTAAGCATACAGCTT 240
 QY 347 GCGGATTTCAAGAGCTTCAAGCTGAACTTGATGGAAGGCTTGTGCTGTGATGACAA 406
 Db 241 GCGGATTTCAAGAGCTTCAAGCTGAACTTGATGGAAGGCTTGTGCTGTGATGACAA 300
 QY 407 AGCAGCTTATGCTTACTATGAGACTATGAGCTTATGAGCTTATGAGAGCTGACAA 466
 Db 301 AGCAGCTTATGCTTACTATGAGACTATGAGCTTATGAGCTTATGAGAGCTTATGACAA 360

QY 467 CTCTGTGTAATGACAGTAGTTTGTAGAGACAAGATTTGAGGAAACAATTAAGAACT 526
 Db 361 ATGCTTGTGACCGATGACGATTTTGAATTAAGATTTGAGGAAACAATTAAGAACT 420
 QY 527 GTCAAGCTTATGCTTGAATTTAGAGGTTATTCATTTTCAATGAGAAATGATGATTAAGC 586
 Db 421 GTCAAGGAGATGCTAGAGATGAGGTTATTCATTTTCAATGAGAAATGATGATTAAGC 480
 QY 587 ACCGAGAGAGCCCATATCAGATTTCTGTGATTTTCTGGGATTAAGATTAAGTATGCT 646
 Db 481 ACTCCAGAGCCCATATCAGATTTCTGTGATTTTCTGGGATTAAGATTAAGTATGCT 540
 QY 647 GCTCTACTGCGGTGGAATGAACTGAAGCTGATTTCTGATTTCTTCTGAGCGATGTTAAAGT 706
 Db 541 GCTCTCTGCGGTGAGCTGAAGCTGATTTCTGATTTCTTCTGAGCGATGTTAAAGT 600
 QY 707 CTTTACAGAGCCCTCCAGATGATTTCTTACTCAAAAGTTGATTCACACTTTTGTAAAGAA 766
 Db 601 CTTTACAGTGGCCCTCCAGATGATTTCTTACTCAAAAGTTGATTCACACTTTTAAAGAA 660
 QY 767 AAACATCAAGATGAGATTAATTAAGTCTGAGAGAGTCAAGATTAAGGAGGAGGATGATGCT 826
 Db 661 AAACACCGAGAGATTAATTAAGTCTGAGAGAGTCAAGATTAAGGAGGAGGATGATGCT 720
 QY 827 GCAAAAGTCAAAAGCTGAGTCAATGACAGCTTATGCTGAGATTTCTGATCAATTAAGCAGT 886
 Db 721 GCAAAAGTCAAAAGCTGAGTCAATGACAGCTTATGCTGAGATTTCTGATCAATTAAGCAGT 780
 QY 887 GGGATTAAGCTGAGATTAATTAAGTCTGAGAGAGTCAAGATTAAGGAGGAGGATGATGCT 946
 Db 781 GGGATTAAGCTGAGATTAATTAAGTCTGAGAGAGTCAAGATTAAGGAGGAGGATGATGCT 840
 QY 947 CATCAAGATGCTGTTATGAGGCTCGATCAAGATTTCTAATGCTGCTGATCATGAGCAGTT 1006
 Db 841 CATCAAGATGCTGTTATGAGGCTCGATCAAGATTTCTAATGCTGCTGATCATGAGCAGTT 960
 QY 1007 GCTGAGAGGAGAAAGTTCAGAAAGCTTCAAGGCTTATCTTCCGAAAGCAGAGAAATTAAT 1066
 Db 901 GCTGAGAGGAGAAAGTTCAGAAAGCTTCAAGGCTTATCTTCCGAAAGCAGAGAAATTAAT 960
 QY 1067 CTGCTTGAATGTCGATGAGGCTTGAAGCAATGTTCTAATCAAAAGCTGAGAAATGAG 1126
 Db 961 CTGCTTGAATGTCGATGAGGCTTGAAGCAATGTTCTAATCAAAAGCTGAGAAATGAG 1020
 QY 1127 TTAAATGATGCTTGTGACAGAGAGGCTGGGTGGAAGATGATGATGCTGCTGATGAT 1186
 Db 1021 TTAAATGATGCTTGTGACAGAGAGGCTGGGTGGAAGATGATGATGCTGCTGATGAT 1080
 QY 1187 ATGACACCTGGAAGATCTGAGGCTTGAAGCAATGTTCTAATCAAAAGCTGAGAAATGAG 1246
 Db 1081 ATGACACCTGGAAGATCTGAGGCTTGAAGCAATGTTCTAATCAAAAGCTGAGAAATGAG 1140
 QY 1247 GATCAATCGGCGCTGTTTAAAGAAACAAGGTGCAAGATGCTTGTCTTGAAGAG 1306
 Db 1141 GATCAATCGGCGCTGTTTAAAGAAACAAGGTGCAAGATGCTTGTCTTGAAGAG 1200
 QY 1307 ACCATCAACCATTAAGGCTGATCTGATGTTTGAATCCGAGCCTGATGATGATGAT 1366
 Db 1201 ACCATCAACCATTAAGGCTGATCTGATGTTTGAATCCGAGCCTGATGATGATGAT 1260
 QY 1367 CAGATAGCTTACCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1426
 Db 1261 CAGATAGCTTACCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 QY 1427 GCCGCGGATCAAAATGCTATCTTACACAGAGTATCTAATGATTAATTCAGAGAGCTGAT 1486
 Db 1321 GCTGCTGATCAAAATGCTATCTTACACAGAGTATCTAATGATTAATTCAGAGAGCTGAT 1380
 QY 1487 GGGGGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1546
 Db 1381 GGGGGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1547 GATGACGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606

Db 1441 GATGACGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 QY 1607 AATGATCAAAATATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1666
 Db 1501 AATGATCAAAATATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 QY 1667 AAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726
 Db 1561 AAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1727 GCAGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
 Db 1621 GCAGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 QY 1787 CTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
 Db 1681 CTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 QY 1847 GCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1906
 Db 1741 GCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 QY 1907 GCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1966
 Db 1801 GCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 QY 1967 GGGAGTGAACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2026
 Db 1861 GGGAGTGAACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 QY 2027 CGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2086
 Db 1921 CGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 QY 2087 CGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2146
 Db 1981 AGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 QY 2147 GTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2206
 Db 2041 GTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 QY 2207 GACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2261
 Db 2101 GATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2145

RESULT 5
 US-09-938-842A-1866
 Sequence 1866, Application US/09938842A
 Publication No. US2004009476A9
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeff
 APPLICANT: Kreps, Joel
 APPLICANT: Wang, Xun
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 FILE REFERENCE: SAME, AND METHODS OF USE
 CURRENT APPLICATION NUMBER: US/09/938, 842A
 PRIOR FILING DATE: 2001-08-24
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 PRIOR APPLICATION NUMBER: US 60/300, 111
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO 1866
 LENGTH: 2181
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana

US-09-938-842A-1866

Query Match 64.9%; Score 1669.8; DB 11; Length 2181;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 297; Indels 0; Gaps 0;

107 ATGAGAGCTAATGATGCTGCTTTGCGAGAGAGCTCAAAAGCTATGCTGCTAG 166
1 ATACAGAGATCATGCTTCAAGCGCTTCCCAAGAGCTTAAAGCTATGCTGCTCAAG 60
167 GTTGGAGCAGCAGCTTTTACTGGAAGAGTGGAGTGGCTTTGGTGGTTAGAGCA 226
61 GTTGGAGCTGCACTTTTACTGGAAGAGTGGAGTGGCTTTGGAGCTTTAGAGCT 120
227 CTGTGGAACAGCTTGGGAAATTAATCTGGAGATTTGAGTGAATGATGCTGCT 286
121 ATCTGGAACAGCTTGGGAGTGAATCTGAGATTTGAGTGAATGATGCTGCT 180
287 GGTGGAGTGGCTTGGAGAGGAGGCTTCTTATGCAATTAATGATGCTGCT 346
181 GTTGGAGTGGCTTGGAGAGGAGGCTTCTTATGCAATTAATGATGCTGCT 240
347 GGGGATCTTCAAGAGCTCAGACTGATGATGGAAGGCTTGGCTGGTGGAGCA 406
241 GCAATTTTCAAGAGGCAAAATGAACTTGAATGGAGAGCTTGGCTGGTGGAG 300
407 AGCAGCTTATGAGCTTATGAGACTATGATTTGACAGCTTGAATGAGAGCTCA 466
301 AGAGCTCATGCTTACTATGAGACTATGATTTGACAGCTTGAATGAGAGCTCA 360
467 CTCTGAGTGAATGAGAGTGAATTTAGAGCAAGATTTGAGAGCAATTAATGA 526
361 ATGCTTGTATGAGCTTATGAGAGTGAATTTGAGAGCAATTAATGA 420
527 GTCAATGATATGATTTGAGAGGCTTATGCAATTTTCAATGAATGAATGCTT 586
421 GTCAAGAGCTGATGAGAGTGAATTTGCAATTTTCAATGAATGAATGCTT 480
587 ACCGAGAGAGCCCATATGAGAGTCTTCTGATTTTCTGGAGTGAAGAGCTT 646
481 ACTGAGAGAGCCCATATGAGAGTCTTCTGATTTTCTGGAGTGAAGAGCTT 540
647 GCTCTATGAGCTTGAAGTGAAGTGAATTTCTGATTTTCTGAGAGTGAAGT 706
541 GCTCTATGAGCTTGAAGTGAAGTGAATTTCTGATTTTCTGAGAGTGAAGT 600
707 CTCTACAGAGCCCTCAAGTATCTTCAATGATGATGATGATGATGATGATG 766
601 CTCTACAGAGCCCTCAAGTATCTTCAATGATGATGATGATGATGATGATG 660
767 AAACATCAAGATGATTAATTTCTGAGCAAAATCAAGATTTGAGAGAGGAGT 826
661 AAACATCAAGATGATTAATTTCTGAGCAAAATCAAGATTTGAGAGAGGAGT 720
827 GCAAAAGTCAAAAGCTCAGTCAATGAGTGAATGAGTGAATGAGTGAATGAGT 886
721 GCAAAAGTCAAAAGCTCAGTCAATGAGTGAATGAGTGAATGAGTGAATGAGT 780
887 GGGATTTAGCTGAGAGCAATTAATGCTCAGAGCAATGAGTGAATGAGTGAAT 946
781 GGGATTTAGCTGAGAGCAATTAATGCTCAGAGCAATGAGTGAATGAGTGAAT 840
947 CATCAAGATGCTGATTTAGGAGTCCAGATGATGATGATGATGATGATGATG 1006
841 CATCAAGATGCTGATTTAGGAGTCCAGATGATGATGATGATGATGATGATG 900
1007 GCTGAGAGGAGAGTTCAGAAAGCTTCAAGAGCTTATCTTGGAGAGAGAGAG 1066
901 GCTGAGAGGAGAGTTCAGAAAGCTTCAAGAGCTTATCTTGGAGAGAGAGAG 960
1067 CTGCTTGAATTTGGAGAGTGGCTTGAAGCAATTTTCAATCAATCAAGAGTGA 1126
961 CTACAGAGATTTGGAGAGTGGCTTGAAGCAATTTTCAATCAATCAAGAGTGA 1020

1127 TTAGATGATGCTTCTGCAAGAGCTGAGTGGAGAGTCAATGATGATGATGAT 1186
1021 TTAGATGATGCTTCTGCAAGAGCTGAGTGGAGAGTCAATGATGATGATGATGAT 1080
1187 ATGACCTGGAAGAGTCTGAGAGCTTGGAGAGTGGAGTGGAGTGGAGTGGAG 1246
1081 ATGAGCTGGAAGAGTCTGAGAGCTTGGAGAGTGGAGTGGAGTGGAGTGGAG 1140
1247 GATCAATTCGAGCTGTTTAAAGAGAGAGAGTGGAGAGTGGAGTGGAGTGGAG 1306
1141 GATCAATTCGAGCTGTTTAAAGAGAGAGTGGAGAGTGGAGTGGAGTGGAG 1200
1307 ACCCTATCAGATTAAGAGCTTCTGATGATGATGATGATGATGATGATGAT 1366
1201 ACCCTATCAGATTAAGAGTCTTCTGATGATGATGATGATGATGATGATGAT 1260
1367 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1426
1261 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
1427 GCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1486
1321 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
1487 GGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1546
1381 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1547 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606
1441 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1607 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1666
1501 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1667 AAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726
1561 AAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1727 GCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
1621 GCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1787 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
1681 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1847 GCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1906
1741 GCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1907 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1966
1801 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1967 GGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2026
1861 GGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
2027 GCGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2086
1921 GCGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
2087 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2146
1981 AGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
2147 GTGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2206
2041 GTGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100

QY 2207 GACGAGACATGATGATTTTACACCCATCAGACATTCCTCC 2251
DB 2101 GATGAGACATGATGATTTTACACCCATCAGACATTCCTCC 2145

RESULT 6
US-10-424-599-44242
; Sequence 44242, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 44242
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139949C.1
US-10-424-599-44242

Query Match 45.5% Score 1170.4; DB 12; Length 2499;
Best Local Similarity 71.4%; Pred. No. 0;
Matches 1590; Conservative 0; Mismatches 591; Indels 45; Gaps 2;

QY 103 GATATGAGAGAGCTAATGCTTCACTGCTTTTCCAGAGAGCTCAACGTAATCGTCT 162
DB 55 GAGATGAGAGAGAGCTAATGCTTCACTGCTTTTCCAGAGAGCTCAACGTAATCGTCT 114

QY 163 TAAGTTGGGACACACAGTTGTTACTGAGAAAAGTGGAAGTGGCTTGTGCTTTAGG 222
DB 115 CAAGTTGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 174

QY 223 AGCACTGCTGAGAGAGCTTGGAGATTTAACTCGAGATGATTTGAGTGTATTTGCTG 282
DB 175 GCACTGCTGAGAGAGATTTAGAGAGCTGATTTCTGTTTATGAGATTTTGTGCTG 254

QY 283 ATCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 342
DB 235 ATCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 294

QY 343 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 402
DB 295 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 354

QY 403 ACAAGAGCTTTATGCTTACTATGAGACTATGCTTATGCTTATGCTTATGCTTATG 462
DB 355 ACAAGAGCTTTATGCTTACTATGAGACTATGCTTATGCTTATGCTTATGCTTATG 414

QY 463 TCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
DB 415 TCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 474

QY 523 AACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
DB 475 AACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 534

QY 583 TAGACCCGAG 642
DB 535 TAGACCCGAG 594

QY 643 AGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
DB 595 AGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654

QY 703 AGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762

DB 655 GAGTCTTATGAG 714
QY 763 AGAAAAACATCAAGATGATTTTACATTCGCGACCAATCAAGATTTAGAGAGAGAGAG 822
DB 715 GAAAAAGCATCAAGATGATTTTACATTCGCGACCAATCAAGATTTAGAGAGAGAGAG 774

QY 823 GAGTCCAAAGATCAAGATGATTTTACATTCGCGACCAATCAAGATTTAGAGAGAGAG 882
DB 775 GAGTCCAAAGATCAAGATGATTTTACATTCGCGACCAATCAAGATTTAGAGAGAGAG 834

QY 883 CAGTGGATTTACAGCTGAGAAACATGATTAAGTCTTCAAGAGAGAGAGAGAGAGAG 942
DB 835 TAGTGGTATGAG 894

QY 943 GTTTCATCAAGATGCTGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1002
DB 895 GTTTCATCAAGATGCTGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 954

QY 1003 AGTTCGCTGAG 1062
DB 955 AGTTCGCTGAG 1014

QY 1063 AATTCTGCTGATTTATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1122
DB 1015 AATTCTGCTGATTTATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1074

QY 1123 TGAGTTAGATGATGCTTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1182
DB 1075 TGAGTTAGATGATGCTTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1127

QY 1183 AGTTATGACACCTGGAAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1242
DB 1128 AGTTATGACACCTGGAAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1176

QY 1243 GGAAGATCCATTCGAG 1302
DB 1177 GGAAGATCCATTCGAG 1236

QY 1303 GAAAGCTCATCAGATGAG 1362
DB 1237 GAAAGCTCATCAGATGAG 1296

QY 1363 TGTACAGATGATGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1422
DB 1297 TGTACAGATGATGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1356

QY 1423 GAGAGCCGAG 1482
DB 1357 GAGAGCCGAG 1416

QY 1483 TGTTCGAGATGATGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1542
DB 1417 TGTTCGAGATGATGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1476

QY 1543 GCTTATGAG 1602
DB 1477 GCTTATGAG 1536

QY 1603 AAAAAATCAAAAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1662
DB 1537 AAAAAATCAAAAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1596

QY 1663 GAG 1722
DB 1597 GAG 1656

QY 1723 TCCAG 1782
DB 1657 TCCAG 1716

QY 1783 TGTTCATGAG 1842

Db 1717 TTGGCTCATAGTATTATTATTGACCTACGACAGAAAGGTGTACATTGTATGGAGACC 1776
 QY 1843 AAGGCAAGTAAAGTACTGACATACGAGACGCGTCACTTCAACCATAGATCTGTC 1902
 Db 1777 CAAGCAGAGCTCTTGTAAATATTCAGATGCTCGATGTACATATAGATCAATTC 1836
 QY 1903 CAAGCTTGCATCTGTGAAGTTGTAGAAGAGCTTATGCTATATGATCACTTCCG 1962
 Db 1897 GTTGGCATGACCAAGTAAATGTGTATGATGATTTATGACGATATGATATTAATCT 1896
 QY 1963 ACATGGGAG-----TGCAACACAGACTGCATTTGTAC 1995
 Db 1897 TTATGGAAGGATCCCACTTTATTTCTGTATATTTGACATATGATTCCTGTTGTC 1956
 QY 1996 AGAGATCATCAGAGTTGACAGAGTATTCCTTCCGCAAGTGGATGCGCTGTGTTCCA 2055
 Db 1957 AGAAGATATATAGATGACCAATGTGTTTCTACGCAAGTACAGATGCTGCTGTTTCCA 2016
 QY 2056 CAAGCCAGACAAAGATTTTCAGATGTTTCCGATTTGCACTTGTGACAGAGTGGGGGT 2115
 Db 2017 CAATGCTAGTACAAAGATTCAGATGATGGGACGATTTGCACTAGTGCAGAGTTGGAA 2076
 QY 2116 AAGCAGGCGAGATTCAGATGCTGATGTCAGATGCGGGTGGAGATTACTTCAACAGAG 2175
 Db 2077 AAGTACAGACAGATTCATGCTCGGGGTCCAGTACGAGTGTGATGATTTTAAACACAG 2136
 QY 2176 ATGATATATGAGAGAAAGACAAAGTGTGACAGAGACATAGAAATTTGTACACCA 2235
 Db 2137 ATGATTTCTCAAGAGAGTGAACAATAGTATGATGATGACAAAGCAATGATACACTCA 2196
 QY 2236 TCAGAGACTTCCCATCCAGTTTAAACAAGCTTCCAGATGTGTGTTGTGATTTGGTT 2295
 Db 2197 CAGAGACTTGGGCTAAAGTTGTAACAATTCAGTGGAGAGAGATTTATGCTATCTGT 2256
 QY 2296 GAGACT 2301
 Db 2257 GCTGCT 2262

RESULT 7

US-10-026-767-1
 : Sequence 1, Application US/10026767
 : Publication No. US20030014774A1
 : GENERAL INFORMATION:
 : APPLICANT: Hitachi, LTD.
 : APPLICANT: RIKEN
 : APPLICANT: Japan International Research Center for Agricultural Science
 : APPLICANT: Bio-oriented Technology Research Advancement Institute (BRAINI)
 : TITLE OF INVENTION: Transgenic rice plant and its family with environmental
 : stress resistant by proline accumulation of high level and its
 : TITLE OF INVENTION: Production.
 : FILE REFERENCE: NT01P0353
 : CURRENT APPLICATION NUMBER: US/10/026,767
 : CURRENT FILING DATE: 2001-12-27
 : NUMBER OF SEQ ID NOS: 3
 : SEQ ID NO 1
 : LENGTH: 2549
 : TYPE: DNA
 : ORGANISM: Oryza sativa L.
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 99..2249
 : PUBLICATION INFORMATION:
 : AUTHORS: Yumiko Igarashi, Yoshu Yoshida, Yukika Sanada, Kazuko
 : AUTORS: Yamaguchi-Shinozaki, Keisiro Wada, Kazuo Shinozaki
 : TITLE: Characterization of the gene for 1-pyrroline-5-carboxylate
 : TITLE: synthetase and correlation between the expression of the gene and
 : TITLE: salt tolerance in Oryza sativa L.
 : JOURNAL: Plant Molecular Biology
 : VOLUME: 33
 : PAGES: 857-865
 : DATE: 1996-12-03
 : DATABASE ACCESSION NUMBER: D49714

: DATABASE ENTRY DATE: 1995-03-16
 : US-10-026-767-1

Query Match 42.2%; Score 1085.6; DB 14; Length 2549;
 Best Local Similarity 69.1%; Pred. No. 0;
 Matches 1484; Conservative 0; Mismatches 664; Indels 0; Gaps 0;

QY 107 ATGAGAGAGCTAGTACGTCTTTCAGTCTCTTTCAGAGAGCGTCAACGATATGCTGCTAG 166
 Db 99 ATGCGAGCGTGCACCCGTCCTCGAGCTTCGTGAGGAGCGTGAACGCGTCACTACAG 158
 QY 167 GTTGGACAGCAGTTGTTACTGAAAGAGTGAAGATTTGCTGCTGTTTACAGCA 226
 Db 159 GTGGGACAGCAGTTGCTCCAGACAAAGTGAAGATTTGGCTTGGCAGGGTTGACCT 218
 QY 227 CTGTGTGAACAGCTTGGGAATTAACCTCGATGATTTGAGATGATTTGCTGCTACT 286
 Db 219 CTGTGAGAGCAGTTAAGAACTGTAACCTTTAGATACGAAGTATTTTGTGCTCA 278
 QY 287 GGTGCGTTGCTCTTGGACAGGCAAGGCTGCTGTTATCGAATTAAGTCAATAGCAGCTT 346
 Db 279 GGTGCTGTTGAGATGGGGCGACAGGCACTTAGTACCGGAAGCTTGTCAATAGCAGCTT 338
 QY 347 GCGGATCTTCAGAACCTTCAGACTGAACTTGAATGGAAGGCTTGTGCTGTTGGAACA 406
 Db 339 GCTGATCTGCAAAAGCCACAGATGAGTATGATGAAAGGCTTGTGCGCTGTTGCTCAG 398
 QY 407 AGCAGCTTATGCTTACATGAGACTATGTTGACAGCTTGAATGTACGCGAGCTCA 466
 Db 399 AGTGAAGTATGCTCTTACGATATGTTGTTTAAACAGTGAATGTCTGCTACTCA 458
 QY 467 CTCTGTGATATGACAGTATTTTAAAGACAGATTTTCAAGAAACAATTAAATGA 526
 Db 459 CTCTGTGACCCAGAGATTTTGAAGAACCAAGTTCCGGGAGCACTCACTGAATCT 518
 QY 527 GTCAAGTATAGCTGATTTTGAAGGTTATTCGAATTTTCAATGAAGATGCTATTAG 586
 Db 519 GTTGAATCTTATATGATCTTAAAGTATACCAATTTTAAAGAAATGATGACACTACG 578
 QY 587 ACCGAAAGAGCCCATATCAGATTTCTTGTGATTTTCTGGGATTAACATAGCTTACT 646
 Db 579 ACTAAGAAAGGCTCCATATGAGATTCATCTGTATATTCGGGAATATGACAGTTTAC 638
 QY 647 GCTTACTGCGGTTGGAATCTGAAGCTGATCTTCTGATCTTCTGAGGATGTTGAAGT 706
 Db 639 GACCTGTTGGCACTGGAATCTGAAGCTGATCTTCTGATCTTCTGAGATGTTGAAGG 698
 QY 707 CTTTACAGAGCCCTCCAGATGATCTTAACTCAAGTTGATCCACACTTTTGTAAAGAA 766
 Db 699 TTGTATATGTTGTCACCAAGTGAACATCAATCAATCAATCAATCAATCAATCAATCA 758
 QY 767 AAACATCAAGTGAATTAATTTGAGGACAAATCAAGATTTAGGAGAGGGGATATGACT 826
 Db 759 AAGCATTCAGCAAGAAATCACTTTTGAAGCAAAATCTGTGATGATGAGGAGGATGACA 818
 QY 827 GCAAAAGTCAAGCTGACGATGATGACGCTTATGCTGGGATTTCTGTCATCATACAGT 886
 Db 819 GCAAAAGTGAAGCTGCTGCTTCTGCTTCAATATGCGGACACACTGTGATTTTAAAGT 878
 QY 887 GGGTATCAGCTGAGAACATGATTAATGCTCTGAGAGACTAGCTGTTGAACCTTGT 946
 Db 879 GGGTTGAAAAATCGAGAGATTTTAAAGTCTTATGATGGGAAAAAATTTGATCTCTTT 938
 QY 947 CATCAAGATGCTGTTATGAGGCTCCGATCAAGATTTATGCTGCGGACATGAGCAGTT 1006
 Db 939 CACAAAGATGGAATTTTGTGGAATCATCTTAAGATTTTATCTTCTGATGATGCTGTT 998
 QY 1007 GCTGAGAGGAAAGTTTCAGAAAGCTTACAGCTTATCTTTCGAAAGACAGAAAAAATT 1066
 Db 999 GCGGCAAGATTTGTTCAAGCATCTACAGAAATTTGATCAAGAGAAACGAAAAAGATA 1058
 QY 1067 CTGCTTATTTGCGGATGCGCTTGAAGCAAAATGTTACTACATCAAAAGCTGAAGATGAG 1126

Db	1059	TTGGCTAGATCTTGCAAGATCTTTGGAGCGCAATGAGATTTTAATAGCTGAGATGAA	1111
Qy	1127	TTAGATGTAGCTTCTGCAACAAGGCTGGGTGGAAAGACTCAATGGTGCCTTAGTT	1186
Db	1119	GCTGATGTAGCTGCGGCCCCAAGATTTCTGATATGAGAGCCCTTGTGGTCTGATTTGACT	11776
Qy	1187	ATGACACCTGAAAGAATCTCGAGCCTTGACGTTAGTTCGTATAGCTAGCTAATGAA	1244
Db	1179	ATTAATCCAGAAAGATAGCAAGCCTTGAAATCTATTCTGACCTTGCAATATGAA	12313
Qy	1247	GATCCATCGCGCGTGTTTTAAAGAAAACAAGGTGGCAGATGTCCTGTCTTAGAAG	1306
Db	1239	GACCTTATTAACACAGATCTTAAAAAGACAGAGGTGTCGATGATTTAGTTCTTGAGAA	1298
Qy	1307	ACCTCATCAACATTTGGGGTACTCTGATGTTGTTTTGAATCCGACCTGAGCACTTGTA	136
Db	1299	AATCTTGCCCATTTAGTGTCTCTTAATGTGTTTGATCCGACCTGATGCTTGTTGTT	135
Qy	1367	CAGATAGCTTCACTTGCCATCCGATGGTGAATGTCCTTGCTGAAGGTGAAAGAG	142
Db	1359	CAGATTTGCATCTTTGGCAATTCGAGTGGTATATGGCTTCTCTTAAAGGTGAAGAA	1418
Qy	1427	GGCGGCGATTCAAATGCTATCTTAACAAGGTATCACTGATGCAATTCGAGACTGT	148
Db	1419	GCTATCAGATCAACACGATATTGCAATTAAGCTTATPACTGATGCTATTCCTGTATGTT	1478
Qy	1487	GGGGGTAAACCTGATGSACTTGACTTGCACTTCAAGAGAAGATTCCTGATTTGCTTAAGCTT	154
Db	1479	GGTGAATAAATTAATGGCTTGTTHAACATAAGATGAGATGGCAGATTTGCTAAAGCTT	153
Qy	1547	CATGACGTTATGATCTTGTGTATCCCAAGAGAACACACAGCTTGTACTCAGATAAA	1606
Db	1539	GATGATGTCATTTGATCTTGTCCTCCAAAGAGAACTAATATAGCTTGCTCCAAATCAAG	1598
Qy	1607	AATACTACAAAAATCCCTGTGTAGTCACTGCTGATGGATGTGTCATGTAATGTGCAC	1666
Db	1599	GCGTCAACTAGATTTCTGTGTTTGGGCACTGTGATGTGATATGCAAGTATATTTGAC	165
Qy	1667	AAAGCTTGATACGATATGCGAAAGCGCATAGTTTCTGATGCAAGTTGGACTATCCA	1726
Db	1659	AAATCAGCTGACATGATATGCGAAACCTTAATGTATGATGATGCAAAACATGATTACCA	1718
Qy	1727	GCAGCTGTAAATGCGATGGAAACCTTCTGTGCAATAAGATCTAGACAGAAATGCTGTG	178
Db	1719	GCGCCTGCATGCATGAGAGCCTTACTAGTTCAATAAGATCTTATTAAGATCCAGGC	1778
Qy	1787	CTTAATGACCTTAATTTTGTGCTGTGCAGACATGAGTCACTTGTATGTGACCAAG	1848
Db	1779	CTTGACGACATATTTAGTGACTTAATAAACAGAAAGATTAAATTTATGTGGACATA	1838
Qy	1847	GCAAGTAAGATATCTGAACATACCAAGACCGGTATTCACCATGAGTACTGTGCGAAG	1906
Db	1839	GCGCAAAAGCTCTGGGATTTCCAAAACCTGTTTATTTCAATCAAGATATAGTCTATG	1898
Qy	1907	GCTTCACTGTGAAATGTGTAGAAACGTTTATGTGCTATPAGATCAATTCACCGACAT	1966
Db	1899	GCGTCACTGTGAAATGTGTGTGATATGTTCAATACGAAATTTGACCAATTTCAATGTTAT	1958
Qy	1967	GGGATGCAACACAGACTGCATTGTACAGAGATCAAGAGTTGCGAGACTATTCCTT	2026
Db	1959	GGAAATGCTCAATACAGATTTGATTCCTCACTACAGATGTAATAGTGTGCGAGACATTTTCTA	2018
Qy	2027	CGCCAAATGATAGAGCTGTGTGTTCCACAACGCGACACAAGATTCGAGATGTTTC	2086
Db	2019	CGCAGATGTATGTGTGTCTGTATTTTCAATATGCAATGACGAATTTCTTGATGGGCT	2078
Qy	2087	CGATTTGGACTTGTGTCAGAGGTGGGGTAAAGCACGGCAGAGATCAATGCTCGTGTGCA	2146
Db	2079	CGTTTGGATTTGGGCTGTGAGGTTGGCATTAAGCACAGGCGATTCATGACCCGTGACCA	2138
Qy	2147	GTCCGGGCGCAAGATTTCAACAACGAGATGATTAATGAGAGAAAAGCAAGTTGTC	2206
Db	2139	GTGGGTGTGAAAGTCTCTTAATCAACAGATGATCTTGCGAGAGCGTGGGCAATGTGTG	2198

Db	968	GAGATGGCAAGCGCGGATTGTACTAGATGCAAAAATATGACTTATCCAGACGGCTGCATCC	909
Qy	1742	ATGAAACCCCTCTCTGTGCAATAAGATCTAGAGCAAAATGCTGTCTTAATAGCTTATT	1801
Db	908	ATGAAATCTCTTCTGTTCAGAGACTGGTAGAAAAGTTGGCTCAATATGATTAATT	849
Qy	1802	TTTGTCTGTGAGAGCAATGAGATCACTTTGTATGTGTGACCAAGGCAAGTAAGTACTG	1861
Db	848	ATTAGACTTACGACAGAGAGGTGTTACATTGTATGAGAGACCCAGGCAAGTCTTTGTTA	789
Qy	1862	AACATACCAAGACAGCGTCATTCAACATAGATCTGTGCGCAAGCTTGCATGTTGAA	1921
Db	788	AATATTCAAATGGCTGTATGTTATCAATCAATGAGTCAAAATTCGTTGCATGCAAGTTGAA	729
Qy	1922	GTGTGTAGAACGCTTATAGGTGTGCTATAGATCACTTACCCGACATGGAGAG-----	1971
Db	728	ATTGTGATGATATGTTTATGTAGAGTATGATATATTAATCTTTATNGAAGCAATGCACT	665
Qy	1972	-----TGACACACAGCTGCATTTGTGAACAGAGATCCAGAAATTGCA	2014
Db	668	CTTATATTTCTTGATTAATTGCAATCTGATTCGCTGTGACAGAAATCAAGATGAAGTACC	609
Qy	2015	GAGCTATTCCTTGGCCAAAGTATGATGCGTGTGTTGCCAACAAGCCAGACAAAGATTC	2074
Db	608	AATGTGTTTCTTACGCCAAGTATGACAGTGTGCTGTGTTTCCAAATGCTATATGTAAGATTC	549
Qy	2075	TCAATGTGTTCCGATTTGCACTTGTTGACGTTGTCAGAGGTGGGGTAAAGCACGGGAGATCCAT	2134
Db	548	AGTATGCGGACACGATTTGCACTTAGGTGCAGAGGTGGATTAAGTAAACAGCAGATTCAT	489
Qy	2135	GCTGTGTGTCAAGTGGGGGTGCAAGAAATTACTTACAAAGAAATGATTAAGAGGAAAA	2194
Db	488	GCTCGGGGTCCAGTATGAGATTTGATGATTTTAAACAACAATGATGATTTCTCAAGGAAAT	429
Qy	2195	GGAACAAGTTGTGACCGACACAATGAAATGTTTAAACCCATCCAGACATTTCCAT	2250
Db	428	GGAACAATAGTGGATGTGACAAACAGTATTAATCACTCACTCACAGAACCTTTCTAT	373

RESULT 9

US-10-425-114-5243

Sequence 5243, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingsong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack B

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 5243

LENGTH: 2447

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700449031_F11

US-10-425-114-5243

Query Match 40.8%; Score 1049.2; DB 12; Length 2447;

Best Local Similarity 67.6%; Pred. No. 8.8e-307;

Matches 1474; Conservative 0; Mismatches 708; Indels 0; Gaps 0;

Qy	91	GACGACGACGACGATTAATGAGAGCTATGATCGTTCACGTCGCTTTGGCCAGAGACGTCAA	150
Db	4	GCGCATGGCCATGAGCCATGAGAGACCGCGCATTCCTGCCCGCATTCGTGTAAAGACGTCAA	63

151 AGGTAACGCTTAAAGTTGGGACAGAGCTTGTACTGAAAAGGTGGAAAGTTGGCTCT 210
Db 64 GGAATCATTTAACAAGTGGGACAGCTGTGTCTGCACTGGCAATGAATGGCCATATGGCCAT 123
Qy 211 TGGTCGTTTAAAGAGCACTGTGTGAACAGCTTGGCAATTAACCTGGATGTATGAGGT 270
Db 124 GGGAGAGCTCGGTTCTCTGTGAACAGGTGAAGCACTGAATTTCAAGGATATGAGGT 183
Qy 271 GATATGTGTATCATCTGTGTGGGCTTGTGTCTTGGCAGGCAAGGCTTGGTATCCAAAT 330
Db 184 GATTCGTGTACCTCAAGAGCTGTGTGTGGGAGCAAGGCTCCAAATCCGTAACCT 243
Qy 331 AGTCATAGCAGCTTGGCGGATCTTCAGAGGCTCAGACTGAATTTGATGGGAAGGCTTG 390
Db 244 TATCCATAGCAGCTTGGCGGATCTTCAGAGGCTCAGACTGAATTTGATGGGAAGGCTTG 303
Qy 391 TGTGTGTGTGAACAAGAGCTTATATGCTTACTATGAGACTATGTTTGAACAGCTTGA 450
Db 304 TGTGTGTGTGTGAACAAGAGCTTATATGCTTACTATGAGACTATGTTTGAACAGCTTGA 363
Qy 451 TGTGACGGGAGCTCAACTCTGTGTATGACAGTATGTTTGAAGACAGAGATTTCAAGAA 510
Db 364 TGTGACGTATCTCAACTCTGTGTATGACAGTATGTTTGAAGACAGAGATTTCAAGAA 423
Qy 511 GCAACTTAAAGAACTGTCAAGCTTATGCTTGAATTTGAGGTTATCCAAATTTCAATGA 570
Db 424 CAGGCTCCGTGAGCTGTGTGTCTTCACTGTATGATCTTAAAGTATGATCCCTATTTAAATGA 483
Qy 571 GAATATGTCTATGACACCCGGAAGAGCCCAATGAGATTTCTGTGTATTTCTGGGA 630
Db 484 GAATATGTCTATGACACCCGGAAGAGCCCAATGAGATTTCTGTGTATTTCTGGGA 543
Qy 631 TAAAGATAGCTTAAAGCTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
Db 544 TAAAGATAGCTTAAAGCTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
Qy 691 GAGGCAATGTGAAGCTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 750
Db 604 TAAAGATAGCTTAAAGCTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Qy 751 CACTTGTGTAAAGAAACATCAAGATGATGATCAATTCGCGCAATCAAGATTAAG 810
Db 664 CACTTGTGTAAAGAAACATCAAGATGATGATCAATTCGCGCAATCAAGATTAAG 723
Qy 811 GAGAGGGGTATGATCTGCAAAAGCTCAAGCTGCAATGCAATGCAATGCAATGCAATGCAAT 870
Db 724 AAGAGGTGCAATGCAAAAGCTCAAGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 783
Qy 871 TGTATCATTAACAGAGGCTTATTCAGCTGAGAACTAATGATTAAGCTCAGAGGACTAG 930
Db 784 TGTATCATTAACAGAGGCTTATTCAGCTGAGAACTAATGATTAAGCTCAGAGGACTAG 843
Qy 931 TGTGTGAACCTTGTGTCAATCAAGATGCTGTGTATGAGGCTCCGATCAGATTTCAATGC 990
Db 844 GATCGGTACATTTTCCAAATGAAGCAAAATTTGTGGCATGTTCCAAAGGAACTACAGC 903
Qy 991 TGTGTGATGAGAGTGTGTGCGAGGAAAGTTCCAGAAAGCTTCAAGGCTTATCTGGGA 1050
Db 904 CCGAGAGATGAGAGTGTGTGCGAGGAAAGTTCCAGAAAGCTTCAAGGCTTATCTGGGA 963
Qy 1051 AAGACAGAAAGAAATTTCTGTGTATGCTGTGTATGCTGTGTATGCTGTGTATGCTGTGTAT 1110
Db 964 GGAACGCAAAAGATTTCTGTGTATGCTGTGTATGCTGTGTATGCTGTGTATGCTGTGTAT 1023
Qy 1111 CAAAGTGAAGAGT 1170
Db 1024 TATGTGTGAAGATGATGCTGT 1083
Qy 1171 GGT 1230
Db 1084 GGT 1143
Qy 1231 GCTAGCTGATATGGAAGATCCAAATGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1290

Db 1144 AACTGTGACATGAGAGACCTTATTTCCATGATCAATGAAAAGACAGAGGTGTCTAAGA 1203
Qy 1291 TCTTGTCTTAAAGAAACCTCATCACATTAAGCGCTTCTGATTTTGAATCCCG 1350
Db 1204 TCTGTTTTTGAAGAAAGCATATGCGCATTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1263
Qy 1351 ACCTGATGACCTTGTACAGATAGCTTCACTTGGCATCCGTAGTGAATGTCTTCTGCT 1410
Db 1264 TCTGATGACCTTGT 1323
Qy 1411 GAAAGGTGAAGAGAGGCGCGGATCAATGCTTCTTCAACAAGTGTATCATGATGC 1470
Db 1324 GAAGAGAGGAAAGAGATGATGAGATCAATGATCAATATTAACAAGTGTATCATGATGC 1383
Qy 1471 AATTCAGAGACTGTGGGGTAACTCATTTGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1530
Db 1384 CATTCAGATGATGCTGTGGGAAAGCTCATGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1443
Qy 1531 TGAATTTGCTTAAAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1590
Db 1444 TGAATTTGCTTAAAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1503
Qy 1591 TGTACTCAGATTAAGAAATTAATAAATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1650
Db 1504 AGTCTCCCAATCAAGCAACAACTAAGATTCAGATTTAGGCTCATGCTGATGATGATGATGATG 1563
Qy 1651 TCAATGATATGCTGCAAGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1710
Db 1564 CCAATGTTTACATTTGAACAAATCAACCGCATGATGATGATGATGATGATGATGATGATGATG 1623
Qy 1711 AAGGTGACATTCAGAGAGCTGT 1770
Db 1624 TAAAGATTTGATTCAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1683
Qy 1771 AAGGCAATGCTGT 1830
Db 1684 TAAAGATTTGATTCAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1743
Qy 1831 GTATGTGACCAAGAGGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1890
Db 1744 TTAATGTGAGCTGT 1803
Qy 1891 TGAATCTGT 1950
Db 1804 TGAATCTGT 1863
Qy 1951 TCAATTTCAACGATGAGAGT 2010
Db 1864 TCAATTTCAACGATGAGAGT 1923
Qy 2011 TGAAGCTATTTCTGT 2070
Db 1924 TGAAGCTATTTCTGT 1983
Qy 2071 AATCTGAGATGCTTCCGATTTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2130
Db 1984 GTTTGT 2043
Qy 2131 CAAATGCTGT 2190
Db 2044 AATGCTGT 2103
Qy 2191 AAAAGGCAAGT 2250
Db 2104 TATGTGCAAGT 2163
Qy 2251 CCAAGCTTAAACAGACTTCCG 2272
Db 2164 GCAATGAGGCAATTAACCTCCG 2185

RESULT 10

US-10-425-114-4280
; Sequence 4280, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4280
; LENGTH: 2418
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700352413_FLI
US-10-425-114-4280

Query Match 40.7%; Score 1046; DB 12; Length 2418;
Best Local Similarity 67.5%; Pred. No. 8.2e-306;
Matches 1472; Conservative 0; Mismatches 710; Indels 0; Gaps 0;

QY 91 GAGGACGACGACATATATGAGAGAGCTAGTACGCTTACGCTTTTGGCCAGAGAGCTCA 150
DB 65 GGGCATTGGCCATGAG 124
QY 151 AGGATGCTGCTTAAAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 210
DB 125 GCGAATATATATCAAGTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 184
QY 211 TGGTGTGTTAG 270
DB 185 GGGGAG 244
QY 271 GATATGCTGCTTAAAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330
DB 245 GATTTGTGTAAGTCTGAG 304
QY 331 AGTCAATAG 390
DB 305 TATCCATAG 364
QY 391 TGGTGTGTTAG 450
DB 365 TGGTGTGTTAG 424
QY 451 TGTGAG 510
DB 425 TGTAAAGTCAATCTCAAGTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
QY 511 GCAACTTAAG 570
DB 485 CCAAGTCCGAG 544
QY 571 GAATGATGCTTAAAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
DB 545 GAATGATGCTTAAAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
QY 631 TAAAGTATGCTTAAAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
DB 605 TAAAGTATGCTTAAAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664
QY 691 GAGGATGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 750
DB 665 TAGTATGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 724
QY 751 CACTTTGTTAAAGAAAAATCAAGATGAGATTACCTGGGAGAGAGAGAGAGAGAGAGAG 810

DB 725 CACTATGCTATTAAG 784
QY 811 GAG 870
DB 785 AAG 844
QY 871 TGTATCATTAAG 930
DB 845 TGTATCATTAAG 904
QY 931 TGTATCATTAAG 990
DB 905 GATGATGATCAATTTTCCAG 964
QY 991 TGTATCATTAAG 1050
DB 965 CCGAG 1024
QY 1051 AG 1110
DB 1025 GGAAG 1084
QY 1111 CAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1170
DB 1085 TAGGCTGAG 1144
QY 1171 GGTGCTGCTTAAAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
DB 1145 GGTGCTGCTTAAAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1204
QY 1231 GCTAGCTGATTAAG 1290
DB 1205 AAGCTGAG 1264
QY 1291 TCTTGTCTTAAAG 1350
DB 1265 TCTGCTTAAAG 1314
QY 1351 AACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1410
DB 1325 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1384
QY 1411 GAG 1470
DB 1385 GAAAG 1444
QY 1471 AATTCAG 1530
DB 1445 TATTCAG 1504
QY 1531 TGAATGCTTAAAGTTGGAG 1590
DB 1505 TGAATGCTTAAAGTTGGAG 1564
QY 1591 TGTATCATTAAG 1650
DB 1565 AGTTTCCAAATCAAG 1624
QY 1651 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710
DB 1625 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1684
QY 1711 AAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1770
DB 1685 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1744
QY 1771 AG 1830
DB 1745 TAAAG 1804
QY 1831 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1890

Db 904 TGTTCATGCAAGTGGGTTTGCAACGATAGCATCATTAAGTTCTCAAGCGGAAA 963
 Qy 931 TGTGGAACCTTGTTCATCAAGATGCTGTTTATGAGGCTCCAGATCAAGATTCATAGC 990
 Db 964 GATCGGTACCTTTCCACACGAAACAAATTTGTGGGCAATGTTCCAGAGAACTCAAGC 1023
 Qy 991 TGTGATGATGAGTGTCTCGAGGAGAAAGTTCCAGAAAGCTTCAGGCTTATCTTGCGA 1050
 Db 1024 CCGAGAGATGCGAGTTGCGGCAAGAGACTGTTCCAGGCGTCTACAGAAATGTCATCAGA 1083
 Qy 1051 AAGACGGAAGAAATTTGCTGATATGTCGATGCGGCTTGAAGCAATGTTTACATCAAT 1110
 Db 1084 GBAACGCAACAGATTTGCTGATATGCTGATGCTGAGAGCAATGAGATCAAT 1143
 Qy 1111 CAAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1170
 Db 1144 TAGGTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
 Qy 1171 GGTGCTGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1230
 Db 1204 GGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
 Qy 1231 GCTAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1290
 Db 1264 AACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
 Qy 1291 TCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1350
 Db 1324 TCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1383
 Qy 1351 AACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1410
 Db 1384 TCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1443
 Qy 1411 GAAAGTGAAG 1470
 Db 1444 GAAAGTGAAG 1503
 Qy 1471 AATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1530
 Db 1504 TATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1563
 Qy 1531 TGTATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1590
 Db 1564 TGTATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
 Qy 1591 TGTATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1650
 Db 1624 AGTTTCCCAATCAAG 1683
 Qy 1651 TGTATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710
 Db 1684 CCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1743
 Qy 1711 AAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1770
 Db 1744 TAAAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803
 Qy 1771 AAGAGCAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1830
 Db 1804 TAAAG 1863
 Qy 1831 GATAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1890
 Db 1864 TATAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
 Qy 1891 TAAAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1950
 Db 1924 TAAAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
 Qy 1951 TCAATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2010
 Db 1984 TCAATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043

Qy 2011 TGCAGAGTATTCCTTCGCGCAAGTGAATGAGGCTGCTGTTCCAAAGCGCAGCAAG 2070
 Db 2044 TGCAGAGGCTTCTTCGACCAAGTGAATGATGCTGCTGTTCCAAAGCGCAGCAAG 2103
 Qy 2071 ATTTCAGATGTTTCCGATTTGAGCTTGTGCAAGTGGGGGTTAGACGCGCAGAT 2130
 Db 2104 GTTTGTGATGAGGAGCGCTTTTGGGCTAGGCTGAGGTTGCAATAGTACAGAGCGCAT 2163
 Qy 2131 CCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2190
 Db 2164 ACATGCCCGCAGACCTGTTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2223
 Qy 2191 AAAAGCAAGTGTTCGACGAGACATGATGATGATGATGATGATGATGATGATGATGAT 2250
 Db 2224 TATGTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2283
 Qy 2251 CCAAGCTTAAACAGACTCCG 2272
 Db 2284 GCATGAGGCAATTAATCTCCG 2305

RESULT 13
 US-10-425-114-31146
 ; Sequence 31146, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 31146
 ; LENGTH: 2612
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLB73134D03_FLI
 ; US-10-425-114-31146

Query Match 40.5%; Score 1042.2; DB 12; Length 2612;
 Best Local Similarity 67.7%; Pred. No. 1.2e-304;
 Matches 1461; Conservative 0; Mismatches 698; Indels 0; Gaps 0;
 Qy 96 CAGAGCATATGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 155
 Db 115 CGGCGGCGGTCATGAGCGACCGGAGACAGAGCGGATTTTCATGAGAGCGTCAACCGG 174
 Qy 156 TCGTCGTTAAGTTGGAGACAGAGTTGTTACTGAAAAGAGTGAAGATGAGCTTGTGTC 215
 Db 175 TCATCATCAAGTGGGCACTGCAATGTTGTCAAGAGGATATGGGAGATATCAAGAGCA 234
 Qy 216 GTTTAAGAGCATGTGTGAACAGCTTGCAGAAATTAATCTGAGATGATTTGAGGTATAT 275
 Db 235 ATTTGGTGTCTTCTTGTGAACAGTGAAGATTAATCTGTAGATGATGAGGTATATCA 294
 Qy 276 TGGTTCATCTGATGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 335
 Db 295 TTGTGTCTCAGGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 354
 Qy 336 ATAGCAGCTTGGGATCTTCAGAGCTTCAGACTGAATTTGATGAGGAGGCTTGTGCTG 395
 Db 355 ATAGCAGCTTGGGATCTTCAGAGCTTCAGACTGAATTTGATGAGGAGGCTTGTGCTG 414
 Qy 396 GTTGGAGCAAGAGCTTATGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 455

415 CCGTGGACAGAGTGGCTCCTGCTCTATGATATGATATTACTCACTGATGAT 474
456 CGGAGCTCACTCTGCTGTAATGACAGTAGTTTAAAGCAAGATTTTGAAGAAC 515
475 CCTTTCCCAACTCTTGTGACAGACAGTAGTTTGAATCCAACTTGAAGAGGC 534
516 TTAATGAAGCTGCAAGCTTATGCTTATTTGAAGGTTATTCGAATTTTCAATGAG 575
535 TTCTGAAAGCTGTGAGCTATTAATCTTAAAGTTGACCAATTTTAAAGAAAAG 594
576 ATGCTATTAGACACCCGAAAGACCCCATATCAGATTTCTTGCTGATTTTCTGGAG 635
595 ATGCTATCAGACCAAGAGGCTCCGATAGAGATTCATGCGGTATATTTGGAGTAAG 654
636 ATAGCTTAGCTGCTCTAGCTGGCTTGGAACTGAAAGCTGATCTTCTGATCTTCTGAGCG 695
655 ACACTTTAGCCGGCTTTTGGCTATAGACTTAAAGAGATCTTCTTGTCTTACTCAGTG 714
696 ATGTTGAAGCTTTTACACAGGCCCTTCAAGTGTCTTAACTCAAGTTGATCCACACTT 755
715 ACGTGAATGGCTCTACAGCGCTCCACCTAGTGAACCTCATCAAGATGATCATACAT 774
756 TTGTTAAGAAAACATCAGATGAGTTACATTCGGCGCAAAATCAGATTGAGAGAG 815
775 ACATCAAGATTAATATCATACGAAATTACTTTGGGATTAAGTCACTGTAGGTAGAG 834
816 GGGGATAGCTGCAAAAAGTCAAGCTCAGTCAATGACCTTATGCTGGATTCCTGTA 875
835 GAGGAATGACAGCTTAAAGTAGAGCTGCTCGTGCTTCAAAAGTGGACACCTGTTG 894
876 TCAATACAGTGGGTATTTAGCTGAGAACATAGATTAAGTCTCAGAGACTACGTGTTG 935
895 TTATTAACAGAGTATGCTGATCTGGGAGCATTAAGATTCCTCAAGAGAGAGAGATTG 954
936 GAACCTTGTTCATCAAGATGCTGTTATGGGCTCGCATCAGAGATTTCAATGCTGAG 995
955 GACTCTCTTCAAAAGAGCGCGAGTTTGTGGAGACATCAATGATTTAGTCAATGAG 1014
996 ACATGCAAGTCTGCGCAGAGGAAAGTTCCAGAAAGCTTCAAGGCTTATCTTCCGAAAGCA 1055
1015 AGATGGCTGTTCAGCAAGAGAAAGTTCAGAGGCTCGCAGAAATTTGCTCGCATGAGAC 1074
1056 GGAATAAATTTCTCTGATATTTGCCGATGCCCTTGAAGCAATTTTACTACAAATCAAG 1115
1075 GCATTAATAATTTCTGAGAGCTGCGGATGCTTTGAGAGAAAATGAGAAATCTAATTAAGA 1134
1116 CTGGAATGAGTATGATGATGCTTCTGCAAGAGGCTGGGTTGGAAGTCAATGATG 1175
1135 CCGAGATGAAGCCGATGATGCTGACGCAAGATGCTGATATGAGAAATTTTGTGTTG 1194
1176 CTGCTTATGATATGACACCTGGAAGATCTGAGCCTTGAAGCTTCAATTTCTTAACTAG 1235
1195 ATATATGACCTTAAAGCCAGAGAAAGATACAGCCCTGGAATCATTTGCACTTTTG 1254
1236 CTGATATGAGAGATCAATCGCCGCTGTTTAAAGAAACAGAGAGTGGCAGATGCTTGG 1295
1255 CAGCTATGAGAGACCAATCAACCAATACTCAAAAGAACAGAGATTTGCGAAATTTAA 1314
1296 TCTTAAAGAAAGCTCATCAACATTTAGGCTTCTGATTTGTTTGAATCCGACCTTG 1355
1315 TTTCGGAAGAAACATCATGCTTCTTGGGATTCCTATGATTTTGTGATCCAGAGCTTG 1374
1356 ATGCACTTGTACAGATGCTTCACTTCCATCCGATGAGTGAAGTGGCTTCTGCTGAAG 1415
1375 ATGCTTGTGCTGATGATGATCTTTAGCGATTTGAAAGTGGCAATGCTTCTTAAAG 1434
1416 GTGGAAGAGAGCCCGCGCATCAATGCTATCTTAAACAAAGTGTATCTGATCAATTC 1475
1435 GTGGAAGAGAGCCATGATGATCAAAACAAAGTATTTGATTAAGCTGAGGCAATTC 1494
1476 CAGAGACTGTTGGGGTAAATCAATGAGCTTGTGACTTCAAGAGAGAGATTCCTGAT 1535
1495 CTAGCAAGTGGGTGAAGAACTTATTTGGCTTGTACAGTGAAGAGCAAAATTTGCTGAT 1554

1536 TGCCTAAGCTTGAATGACCTTATTCATCTTGTGATCCCAAGAGAGCAACAGCTTGTTA 1595
1555 TACTAAGCTTCAATGATATATGATCTTGTTCATTCCAAGAGAGCAATATAGCTGTTT 1614
1596 CTGAGATTAATAAATCTCAAAATATCCCTGTGATAGTCACTGATGATGATGATGATG 1655
1615 CACAAATCAAGACATCAATCAATGATCCCTGTCTTGTGATGATGATGATGATGATG 1674
1656 TATATGTCAGCAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1715
1675 TATATGTCAGCAATCAATCAATGATGATGATGATGATGATGATGATGATGATGATG 1734
1716 TGAATCTTCCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1775
1735 TTGATTAACCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1794
1776 AGAATGCTGTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1835
1795 AGGCTCCAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1854
1836 GTGACCAAGAGGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1895
1855 GGGGCTCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1914
1896 ACTGTGCCAAGGCTTGCATGATGATGATGATGATGATGATGATGATGATGATGATG 1955
1915 ATAGTTTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1974
1956 TTACCGACATGAGAGTGCACACACAGCTGATGATGATGATGATGATGATGATGATG 2015
1975 TACATTTGATGAGAGTGCACATGATGATGATGATGATGATGATGATGATGATGATG 2034
2016 AGCTATTCCTTGGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 2075
2035 AAACCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2094
2076 CAGATGCTTCCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2135
2095 CTGACGGGCTGCTGTTTGGATGATGATGATGATGATGATGATGATGATGATGATG 2154
2136 CTGCTGTGTCAGTGGGCTGCAAGATTTACTTACAGAGATGATGATGATGATGATG 2195
2155 CTCGTGGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2214
2196 GACAAATGTCAGAGGACATGATGATGATGATGATGATGATGATGATGATGATGATG 2254
2215 GCGAAGTGTGAACGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2273

RESULT 14
US-10-424-599-44244
Sequence 44244, Application US/10424599
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 44244
LENGTH: 1952
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_139950C.1
US-10-424-599-44244

QY 719 CCTCCAGTATGCTTAACGAAAGTATGATCCAGCTTTTGTAAAGAAAACATCAAGT 778
 DB 62 CCTCCAGTATGCTTAACGAAAGTATGATCCAGCTTTTGTAAAGAAAACATCAAGT 121
 QY 779 GAGATTACATTCGCGCAAAATCAAGATTAGGAGAGGGGTATGACTGCAAAAGTCAMA 838
 DB 122 GAATTAATCTTTGGTGAACAATCTAGAGTGGGAAGGGTGAATGACTGCAAAAGTAAA 181
 QY 839 GCTGACATCAATGAGCTTATGCTGGGATTCCTGTCATCATCAACGATGGGTATTCAGT 898
 DB 182 GCTGCTGTCATGATGATGATGCTGGGATTCCTGTCATCATCAACGATGGGTATTCAGT 241
 QY 899 GAGAACATGATTAAGTCTCAAGAGACTACGTTGGAACCTTGTTCATCAAGATGCT 958
 DB 242 GAGAAATTAATGATGATGCTCAAGAGACTACGTTGGAACCTTGTTCATCAAGATGCT 301
 QY 959 GCTTATGAGGCTCCGATCAAGATTTAATGCTGCTGATCATGGCAGTTGCTGGAGGAA 1018
 DB 302 CATGAGTGGGTCGAAATGAAAGGTTGATGCTGCTGATGATGCTGAGGAGGAA 361
 QY 1019 AGTCCAGAAAGCTTCAGGCTTATCTTGGGAAAGACGAAAAAATTCGCTGATAT 1078
 DB 362 TGTTCAGAAAGCTTCAGGCTTATCTTGGGAAAGACGAAAAAATTCGCTGATAT 421
 QY 1079 GCGGATGCTCTGAGCAAAATGTTACTACATCAAGCTGAGATGATGATGAT 1138
 DB 422 GCTGATGCTCTGAGCAAAATGTTACTACATCAAGCTGAGATGATGATGAT 481
 QY 1139 TCTGCAAGAGGCTGGGTGGAAGATGATGATGATGATGATGATGATGATGATGAT 1198
 DB 482 GTCGCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
 QY 1199 AAGATCTGAGGCTTGCAGCTTCAAGTCTGATGATGATGATGATGATGATGATGAT 1258
 DB 542 AAGATCTGAGGCTTGCAGGCAACATGCAATTAATGCAACATGCAATTAATGAT 601
 QY 1259 CGTGTTTTAAAGAAAACAGAGGTGGCAGATGCTTGTCTTAAAGAAAGCTCATCA 1318
 DB 602 CAATATATTAAGAAAACAGAGGTGGCTAATTTTAAAGAAAGCTCATCTCT 661
 QY 1319 TTAGGCGTACTTGCATTTGTTTGAATCCGACCTGATGCACTTGTAAAGATGCTCA 1378
 DB 662 TTGGAGATGCTCTTATTTGTTTGAATCCGACCTGATGCTTGTAAAGATGCTCA 721
 QY 1379 CTGGCAATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1438
 DB 722 CTGGCAATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 781
 QY 1439 AATGCTATCTTAACAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1498
 DB 782 AATGCTATCTTAACAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 841
 QY 1499 AATGCTATCTTAACAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1558
 DB 842 AATGCTATCTTAACAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 901
 QY 1559 GATTTTGTATCCCAAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1618
 DB 902 GATTTTGTATCCCAAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 961
 QY 1619 ATCCCTGTAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1678
 DB 962 ATCCCTGTAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021
 QY 1679 ACGGATATGCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1738
 DB 1022 GTGGAGATGCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1081
 QY 1739 GCGATGAAACCTTCTTGTGATTAAGATCTAGAGAGGATGATGATGATGATGAT 1798
 DB 1082 GCGATGAAACCTTCTTGTGATTAAGATCTAGAGAGGATGATGATGATGATGAT 1141
 QY 1799 ATTTTGTCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1858

DB 1142 GTTGTGACCTTACCAATGCAAGGCGTTAAATTAATGAGAGCCAAAGGCAAGTCTCTG 1201
 QY 1859 CTGAACATACCAAGAGCGGCTCATTCACCATGATGATGATGATGATGATGATGAT 1918
 DB 1202 TTAATATATCCCAAGAGCAAAACATTTTCATCATGATGATGATGATGATGATGAT 1261
 QY 1919 GAAATGATGAAAGCGTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1978
 DB 1262 GAAATGATGAAAGCGTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
 QY 1979 ACAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2038
 DB 1322 ACTGATCTCATGCTTGCAGAAAGATTAAGAGTTGCTAATGATGATGATGATGATGAT 1381
 QY 2039 AGCGTGTGCTGCTTCCCAAGCCAGAGCAAAAGATTCATGATGATGATGATGATGAT 2098
 DB 1382 AGTGTGCTGTTTTCACAAATGCAAGCAACGATTCAGTATGATGATGATGATGAT 1441
 QY 2099 GGTGCAAGAGTGGGAGTAAAGCAGGAGGATCCATGCTGCTGCTGCTGCTGCTGCT 2158
 DB 1442 GCGCAGAGGTTGGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1501
 QY 2159 GATTTACTTAACAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2218
 DB 1502 GATTTACTTAACAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1561
 QY 2219 GGAATGTTTACACCATCAGAGCATTCCCATCCAAAGCTTAA 2260
 DB 1562 GGAATGTTTACACCATCAGAGCATTCCCATCCAAAGCTTAA 1603

Search completed: March 10, 2004, 11:58:30
 Job time : 849.374 secs

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: March 10, 2004, 10:40:15 ; Search time 5867.85 Seconds
(without alignments)
13084.110 Million cell updates/sec

Title: US-10-026-767-2

Perfect score: 2571

Sequence: 1 ctgctactattcttcttacc.....tcaagatcactactcttc 2571

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1050.4	40.9	2627	13	BUI03703 SCJFR107
2	753.4	29.3	887	10	BR037600 AA01P10 A
3	742.2	28.9	748	14	CB257851
4	730.4	28.4	1961	11	AV109740 Zee maye

5	686.8	26.7	730	10	BE037665
6	671.2	26.1	676	14	BE037689
7	668.6	25.9	806	12	BM985508
8	654	25.4	654	14	CB257853
9	653.4	25.4	1685	11	AY105865
10	639.2	24.9	698	10	BE037874
11	619	24.1	619	9	AV560359
12	612	23.8	648	14	CB257169
13	596.4	23.2	598	9	AV523699
14	591.8	23.0	595	14	CB258886
15	570.8	22.2	591	13	BU635444
16	551.4	21.4	835	14	CB686249
17	544	21.2	554	14	CB255735
18	541	21.0	542	9	AV440610
19	540.4	21.0	567	9	AV831177
20	524	20.4	542	14	CB257848
21	519	20.2	592	9	AV826224
22	518.2	20.2	876	13	BU238245
23	512.4	19.9	649	14	CB829418
24	512	19.9	512	9	AV529336
25	487.4	19.0	697	14	CB837716
26	484.8	18.9	529	14	CB257595
27	471	18.3	495	9	AV784532
28	470.8	18.2	774	14	AV552988
29	467.2	18.2	770	14	CB349405
30	451.2	17.5	801	14	CB291717
31	449.4	17.5	451	9	AV794408
32	443	17.2	674	9	AV823133
33	439.4	17.1	441	9	AV795491
34	435.2	16.9	785	14	CB292847
35	435	16.9	435	9	AV794702
36	432.8	16.8	667	9	AB050546
37	431.4	16.8	434	9	AV796385
38	430.8	16.8	701	13	BU862253
39	426.8	16.6	451	9	AV793771
40	426	16.6	743	14	CF208166
41	424	16.5	778	14	CF393964
42	422.8	16.4	437	9	AV807915
43	422.8	16.4	771	12	BI175930
44	418.4	16.3	833	14	CF441807
45	418	16.3	418	9	AV798979

ALIGNMENTS

RESULT 1
BUI03703
LOCUS
DEFINITION
SCJFR1073H12.9 Saccharum officinarum mRNA (Nogueira, F.T.S.)
SACCHARUM OFFICINARUM cDNA, mRNA sequence.
ACCESSION
BUI03703
VERSION
BUI03703.1 GI:32815034
KEYWORDS
SOURCE
ORGANISM
Saccharum officinarum
EST.
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 2627)
Nogueira, F.T.S., de Rosa, V.E. Jr., Menossi, N., Ulian, E.C. and
Arruda, P.
RNA expression profiles and data mining of sugarcane response to
low temperature
Plant Physiol. 132 (4), 1811-1824 (2003)
22953309
12913139
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Bioinformatics Lab
Organization for Nucleotide Sequencing and Analysis
C.P. 6176, Campinas, SP 13083-970, Brazil
Tel: 55 19 37881101
Fax: 55 19 37881089

FEATURES
source

Email: tedald@unicamp.br.
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 1 (bases 1 to 887)
 Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Bacon, M.,
 Parra, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
 Palacios, C., Scarpa, G., Wiese, M., and Zepeda, G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 Contact: Michalowski, C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: chm@u.arizona.edu
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 1 (bases 1 to 748)
 Schmidt, K.J., Sorensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
 Mitchell-Olds, R., and Weisshaar, B.
 Large-scale identification and analysis of genome-wide
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 Genome Res. 13 (6), 1250-1257 (2003)
 22683290
 MEDLINE 12799357
 PUBMED
 COMMENT
 Contact: Weisshaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mp12-koeln.mpg.de
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REFERENCE
 Bohnert, H.J., Borchert, C., Brazillie, S., Brooks, J., Eaton, M.,
 Ferrera, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
 Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 CONTACT
 Contact: Michalowski, C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: chm@u.arizona.edu
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AUTHORS	1 (bases 1 to 676) Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.						
TITLE	Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana						

JOURNAL
MEDLINE
PUBMED
COMMENT

Genome Res. 13 (6), 1250-1257 (2003)
22683290
12789357

Contact: Weisshar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaempfl-z-koeln.mpg.de

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Location/Qualifiers

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T7-SalI-CCAGCGGTCCG-5prime-cDNA-polyA-CC-NotI-SP6. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weisshar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact gabi.rzpd.de for further information."

ORIGIN

Query Match	26.1%	Score 671.2	DB 14	Length 676
Best Local Similarity	99.6%	Pred. No. 4.8e-162		
Matches 673	Conservative 0	Mismatches 3	Indels 0	Gaps 0

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ACCESSION	BM985508		
VERSION	BM985508.1	GI:19684146	
KEYWORDS	EST.		
SOURCE	Theilungella halophila		
ORGANISM	Theilungella halophila		
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	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;		
	rosids; eurosids II; Brassicales; Brassicaceae; Theilungella.		
REFERENCE	1 (bases 1 to 806)		
AUTHORS	Gong,Z., Zhu,J., Zhang,C., Kim,C.S., Zhang,Q., Bressan,R.,		
TITLE	Hasegawa,M., Zhu,J.R. and Fredricksen,M.A.		
JOURNAL	Transcript profile from Theilungella halophila, a salt-tolerant		
COMMENT	relative of Arabidopsis thaliana		
	Unpublished (2000)		
	Contact: Mark Fredricksen		
	Department of Plant Biology		
	University of Illinois		
	1201 W. Gregory Dr., Urbana, IL 61801, USA		
	Tel: 2172655473		
	Email: bohnertlab@life.uiuc.edu.		
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Dd		95	AGTGGAAATGCTTTCTATTGTGAAGGGTGAAAAGAGGCCCGGCAGTCAAATGCTATCTTA	154
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Dd		155	CATAAGGTGATCACTGTANTGCAATTCGAGAGCTGTGGGGGTAACACTATGTGACTTGTG	214
Oy		1511	ACTTCAAGAGAAGAGATTCCTGATTTGGCTTAACTGTGATGACGTATGCACTTGTGATC	1570
Dd		215	ACTTCAGAGAGAAGAGATTTCCGATTTTGTCTCAAGCTTATGACGTTATGATCTTGTGATC	274
Oy		1571	CCAAAGGAGCAACAAGCTTGTACTCAGATAAAAAAATACTACAAAATCCTGTGCTA	1630
Dd		275	CCAAGAGGCAACAAGCTTGTTCCTCCAGATAAAAAAATACTACAAAATCCTGTGCTA	334
Oy		1651	GGTATGCTGATGGAATCTGTCACTGATATGATGTCACAAGCTTGTGATPAGCGATATGCA	1690
Dd		335	GGCATGCTGATGGAATCTGTCACTGATATGATGTCACAAGCTATATATCTGATATGCA	394
Oy		1691	AAGCGCATAGTTTTCTGATGTCAAAGTTGGACTATCCAGAGCTGTAAATGCGATGAAACC	1750
Dd		395	AAGCGCATATTTCCATGAGCAAGTAGTGAATTATCCAGAGCTGTAAATGCGATGAAACT	454
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Dd		512	CAGAGCATAGGATGCACTGTATATGTGTGAGCAAGAGCAAGTGAATATCTGAACATACCA	571
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Dd		572	GAACACGCTGTCTCACTATGAGTACTGTTCGAAGGCTTGCACTGTGAAATGTGAA	631
Oy		1931	GACGTTATGCTGTATATGATCATTCACATCCGATATGGAGTGCACACAGATGTGACTT	1990
Dd		632	GACGTTATGCTGTATATGATCATATCCGATATGGAGTGCACACAGATGTGACTT	691
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DEFINITION	96-E011802-014-004-O24-TTR MP1Z-ADIS-014 Arabidopsis thaliana cDNA clone MP1ZP711024Q 5'-PRIME, mRNA sequence.			
ACCESSION	CB257853			
VERSION	CB257853.1	GI:32882626		
KEYWORDS	EST.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weishaar,B. Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)			
AUTHORS	Contact: Weishaar B			
JOURNAL MEDLINE PUBMED	ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-Von-Linne Weg 10, 50829 Koeln, Germany			
COMMENT				

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FEATURES
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QY	306	GGCAAGGCTTCGTTATCGACAATTATGTCATATGACGCTTTGCGATCTTCAGAA	355
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QY	366	AGACTGAACCTTATGGGAAGCGCTTGCTGCGTGTGGACAAGAAGCTTTATGGCTTACT	425
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QY	426	ATGAGACTATGTTGACACAGCTTGAATGTCACGGACGCTCAACTCTGGTGATACAGTA	485
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QY	486	GTTTATAGACAGAAGATTCACGAAGCACTTATGAACCTGTCAAGTCTATGCTTGATT	545
Db	241	GTTTATAGACAGAAGATTCACGAAGCACTTATGAACCTGTCAAGTCTATGCTTGATT	300
QY	546	TGAGGGTATTCCAATTTTCAATGAGATGATGCTATTAGACCCGGAAGACCCCATATC	605
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QY	606	AGGATCTTCTGGATTTTCTGGGAATAGATATGCTATGCTGCTACTGCGCTTGAAC	665
Db	361	AGGATCTTCTGGATTTTCTGGGAATAGATATGCTATGCTGCTACTGCGCTTGAAC	420

Qy	666	TGAAACCTATCTCTGATCTCTCTCGAACGANTGTGAAGGCTTTAACAGGGCCCTCCAA	725
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Qy	726	GTGATCCTAATCAAGTTGATCCACATTTTGTATAAGAAAAATCAAGATGAGATT	785
Ds	481	GTGATCCTAATCAAGTTGATCCACATTTTGTATAAGAAAAATCAAGATGAGATT	540
Qy	786	CATTGGGCGAATTCAGATTAGGGAGAGGGGGTATGATCTGCAAAAGTCAAAGCTGCAG	845
Ds	541	CATTGGGCGAATTCAGATTAGGGAGAGGGGGTATGATCTGCAAAAGTCAAAGCTGCAG	600
Qy	846	TCATGCACTTATCTGTGGATTCCTGTATCATTAACAGTGGGTATTCACGCTG	899
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LOCUS	AY105865
DEFINITION	AY105865 Zee mays PC0085448 mRNA sequence.
ACCESSION	AY105865
VERSION	AY105865.1 GI:21208943
KEYWORDS	HTC.
SOURCE	Zee mays
ORGANISM	Zee mays

FEATURES

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Db	131	CAGAGTTGTCAATCAGAGAGAGCAAAAGATTTTGTAAGATATTTGCTGATGCTTCGGA	190
Qy	1094	GCAATGTTACTACATCAATCAAGCTGAGATGAGTAGTAGTGTGCTTCGACCAAGGCT	1153
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Qy	1154	GCGTTGGAAGAGTCAATGCTGCTCGCTTAGTTATGACCTGGAAGATCTCGAGCTT	1213
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Qy	1274	ACAGAGTGGCAGATGCTGTGTCTTAAAGAAAGCTATCAACATTAAGGCTACTTCTG	1333
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Qy	1334	ATTGTTTGAATCCCGACCTGATGCCACTTGTACAGATAGCTTCACTTGGCATCCGTAGT	1393
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Db	611	AGCAAGAGGAATTGCTGATCTTACAGCGCTGATGATGATTAATGATCTTGTCAATCCG	670
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Qy	1814	AGCATGAGTCACTTTGTATGTTGACCAAGGGCAATTAAGATCTCAATCCAGAA	1873
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Qy	1874	GCACGGTCATTCAACCATGAGTACTGTGCCAAGGCTTGCACTGTTGAAGTTGTGAAGAC	1933
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Db	1031	GTCAGTCAAGCTATGATCACTAATATGTTATGGAATGCAACAACAGATCGATCAATC	1090
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QY	2234	CATCAGGACATTTCCCATCCAAAGCTTAAACAAGACTTCG	2272
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RESULT 10	
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ACCESSION	AA05P09
VERSION	BE037874.1
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ORGANISM	Arabidopsis thaliana (thale cress)
REFERENCE	Arabidopsis thaliana (thale cress) Eukaryotes/Viridiplantae/Streptophyta/Embryophyta/Tracheophyta; Spermatophyta/Magnoliophyta/eudicotyledons/core eudicots; rosids/eurosid II/Brassicales/Brassicaceae/Arabidopsis. 1 (bases 1 to 698)
AUTHORS	Bohnert,H.J., Borchert,C., Brazille,S., Brooke,J., Eaton,M., Farrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R. Functional genomics of Plant Stress Tolerance Unpublished (2000) Contact: Michalowski,C.B.

University Of Arizona
 BIO Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu
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 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE
 AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size-selected cDNA libraries
 JOURNAL DNA Res. 7 (3), 175-180 (2000)
 MEDLINE 20363092
 PUBMED 10907847
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
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Best Local Similarity 100.0%; Pred. No. 14e-148;
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 QY 1053 ACAGAAAAAATTCCTGCTGATATATCCGATGCTCCGATCAAAATGTACTACATCA 1112
 DB 121 ACAGAAAAAATTCCTGCTGATATATCCGATGCTCCGATCAAAATGTACTACATCA 180
 QY 1113 AAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1172
 DB 181 AAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 1173 TGGCTGCTAGTTATGACACCTGGAAGATCTCGAGCTTGCAGCTTCACTGTAAGC 1232
 DB 241 TGGCTGCTAGTTATGACACCTGGAAGATCTCGAGCTTGCAGCTTCACTGTAAGC 300
 QY 1233 TAGCTATATGAGAGATCCATATGCGCTGTTTAAAGAAAAGAGGTGCGAGATGCTC 1292
 DB 301 TAGCTATATGAGAGATCCATATGCGCTGTTTAAAGAAAAGAGGTGCGAGATGCTC 360
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 DB 361 TTGCTTAAAGAAAGCTCATACCAATGAGGATCTGATGTTGTTTGAATCCGAGC 420
 QY 1353 CTGATCCTTGTACAGATAGCTTCACTTCCATCCGATGATGATGATGATGATGATGAT 1412
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 DB 601 ATTGCTTAAAGCTTGAAGA 619

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 LOCUS CB257169 42-E012743-027-007-D11-T7R MP12-ADIS-027 Arabidopsis thaliana cDNA
 DEFINITION clone MP12p772D117Q 5-PRIME, mRNA sequence.
 ACCESSION CB257169
 VERSION CB257169.1 GI:32881942
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE
 AUTHORS Schmidt, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
 Mitchell-Olds, T. and Weisshaar, B.
 TITLE Large-scale identification and analysis of genome-wide
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 JOURNAL Genome Res. 13 (6), 1250-1257 (2003)
 MEDLINE 22683290
 PUBMED 12799357
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851
 Email: weishsha@mpiz-koeln.mpg.de
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 Location/Qualifiers

FEATURES

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ORIGIN

Query Match 23.8%; Score 612; DB 14; Length 648;
 Best Local Similarity 99.5%; Pred. No. 9.3e-147;
 Matches 634; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
 935 GGAACCTGTTTCA-TCAAGATGCTGTTTATGGGCTCCGATCAGATTTAATGCTCG 993
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 994 TGAATGAGGAGTTGCTGCGAGGAGGAGTTCCAGAAAGCTTCAGGCTTATCTTCGAGAA 1053
 72 TGACATGCGAGTTGCTGCGAGGAGGAGTTCCAGAAAGCTTCAGGCTTATCTTCGAGAA 131
 1054 CAGGAGAAATTTCTGCTGATTTATGCCAGATGCTTCAGCAATGTTTCACTCAATCAA 1113
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 1294 TGTCTTAAAGAGAGAGCTTCAATCAGATTTAGCGGCTTCTGATGTTTGTGAAATCCGAGCC 1353
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QY 1354 TGATGCACTTGTACAGATAGTCTGATCTGATCCATCCGATGAGAAATGCTTCTGTGAA 1413
 DB 432 TGATGCACTTGTACAGATAGTCTGATCTGATCCATCCGATGAGAAATGCTTCTGTGAA 491
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 DB 492 GGGTGAAG 551
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RESULT 13

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT

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ORIGIN

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 Best Local Similarity 99.8%; Pred. No. 9.8e-143;
 Matches 597; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 598 GTTGTAG 539
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Oy		2162	TTACTTACAACAGATGGAATAATGAGAGAAAAGACAAGTTGTGACGAGACATATGA	2221
Dd		358	TTACTTACAACAGAGTGAATATGAGAGAAAAGACAAGTTGTGACGAGACATATGA	299
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Dd		238	TGTGTATTTGGTTTGAAGCTTGAGAGAGACACAGAGAGAGATGGGCTTTTTTGTTCCT	179
Oy		2342	CTGCGCTTAGTACATCATNCCATCATATATATATTTCTCACTAATTATTTATGAAACC	2401
Dd		178	CTGCGCTTAGTACATCATNCCATCATATATATATATTTCTCACTAATTATTTATGAAACC	119
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Dd		118	TGCGTTATGTATGTGTTTGTATTTAGATTTAGAGTTGACCAAAAATAAGATCCA	59
Oy		2462	CCACTTACTCTTGCTCATATAGTACATGAAGAAKCTTTATATAGTTCTCTCTGTC	2519
Dd		58	CCACTTACTCTTGCTCATATAGTACATGAAGAAKCTTTATATAGTTCTCTCTGTC	1
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DEFINITION		09-E012732-014-002-A03-T7R MPZ-ADIS-014 Arabidopsis thaliana cDNA		
ACCESSION		CB258886		
VERSION		CB258886.1	GI:32883659	
KEYWORDS		EST.		
SOURCE		Arabidopsis thaliana (thale cress)		
ORGANISM		Arabidopsis thaliana		
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi		
AUTHORS		1 (bases 1 to 595) Schmid,K.v., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B. large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)		
TITLE		Contact: Weisshaar B ADIS DNA core facility at MPZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weisshaar@mpiz-koeln.mpg.de Insert Length: 595 Std Error: 0.00 Plate: 2 row: A column: 03 Seq primer: T7R; CTATACGACTCATATAGGA.		
JOURNAL MEDLINE		PubMed		
COMMENT		Location/Qualifiers		
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VERSION BU635444.1 GI:23302699
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SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 591)
Lundsgaard, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S.
and Welinder, K.G.
EST sequencing of Erysiphe cichoracearum infected Arabidopsis
plants
JOURNAL Unpublished (2002)
COMMENT Contact: Karen G. Welinder
Institute for bioteknologi
Aalborg Universitet
Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk.
Location/Qualifiers
1. .591
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/mol_type="mRNA"
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/db_xref="taxon:3702"
/dev_stage="Plant 3 weeks old, three days post infection"
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/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
library of Arabidopsis and E. cichoracearum infected leaf
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dt
selected."
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Best Local Similarity 99.7%; Pred. No. 4e-136; Indels 0; Gaps 0;
Matches 572; Conservative 0; Mismatches 2;
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Db 1 ACGAGCAGAAAGTTCAGAGCTATTCCTTGCAGAGTATGCGCTGCTGTGTCACA 60
QY 2058 ACGGACGACAAAGTTCAGAGCTATTCCTTGCAGAGTATGCGCTGCTGTGTCACA 2117
Db 61 ACGGACGACAAAGTTCAGAGCTATTCCTTGCAGAGTATGCGCTGCTGTGTCACA 120
QY 2118 GCAAGGACGACATTCAGAGCTATTCCTTGCAGAGTATGCGCTGCTGTGTCACA 2177
Db 121 GCAAGGACGACATTCAGAGCTATTCCTTGCAGAGTATGCGCTGCTGTGTCACA 180
QY 2178 GGATTAATGAAGAGAAAGGAGGAGTTCAGAGTATGCGCTGCTGTGTCACA 2237
Db 181 GGATTAATGAAGAGAAAGGAGGAGTTCAGAGTATGCGCTGCTGTGTCACA 240
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QY 2418 TTGATTTAGGTTAGGATGCAACCAAAATTAAGATCACTTACCACTTAGCTGTGTC 2477
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Db 541 ATTTCTGATCTTTATCAAGATPACTACTTTTC 574
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Job time: 5875.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2004, 10:31:30 ; Search time 6881.99 Seconds

(without alignments)
11544.306 Million cell updates/sec

Title: US-10-026-767-3

Sequence: 1 agcgttcagaaaaaacagc.....ataaaatgcttttacttc 1833

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Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hcg:*
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12: gb_sy:*
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14: gb_vl:*
15: em_ba:*
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17: em_hum:*
18: em_in:*
19: em_mu:*
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41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1833	100.0	1833	8 D83025	D83025 Arabidopsis
2	1825.2	99.6	1841	8 AY074571	AY074571 Arabidopsis
3	1818.4	99.2	1854	8 AF428306	AF428306 Arabidopsis
4	1817.8	99.2	1855	8 ATPOX	X97075 A.thaliana
5	1722.8	94.0	1745	8 ATU59508	U59508 Arabidopsis
6	1490.4	81.3	1500	6 AX651553	AX651553 Sequence
7	1457.8	79.5	1461	6 AX506716	AX506716 Sequence
8	949.4	51.8	82347	8 AB028614	AB028614 Arabidopsis
9	525.6	28.7	669	8 AB097404	AB097404 Arabidopsis
10	479.2	26.1	47460	8 AB011478	AB011478 Arabidopsis
11	441.8	24.1	1872	8 AB046419	AB046419 Nicotiana
12	274	14.9	1782	8 AK121010	AK121010 Oryza sat
13	261	14.2	333	8 AF171226	AF171226 Brassica
14	258	14.1	1227	6 AX653926	AX653926 Sequence
15	240.5	13.1	84914	8 AP006372	AP006372 Lotus cor
16	227.2	12.4	144798	8 AC026758	AC026758 Oryza sat
17	227.2	12.4	304419	8 AE017118	AE017118 Oryza sat
18	170	9.3	1573	8 AB008810	AB008810 Arabidopsis
19	157.8	8.6	417	8 AY327888	AY327888 Medicago
20	151	8.2	2000	6 AX509409	AX509409 Sequence
21	151	8.2	2000	6 AX653724	AX653724 Sequence
22	149	8.1	36034	8 AP001296	AP001296 Arabidopsis
23	145.6	7.9	702	8 ATH524542	AJ524542 Arabidopsis
24	130.4	7.1	2112	10 BC037468	BC037468 Mus muscu
25	130.4	7.1	2228	10 MM080020	U80020 Mus muscu
26	123.6	6.7	1494	6 AR371475	AR371475 Sequence
27	123.6	6.7	2240	6 AR371478	AR371478 Sequence
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32	119.4	6.5	121	6 AX324860	AX324860 Sequence
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35	119.4	6.5	121	6 AX324867	AX324867 Sequence
36	119.4	6.5	121	6 AX324868	AX324868 Sequence
37	117.8	6.4	121	6 AX324855	AX324855 Sequence
38	117.8	6.4	121	6 AX324856	AX324856 Sequence
39	107.2	5.8	1551	6 AR371474	AR371474 Sequence
40	107.2	5.8	2389	6 AR371479	AR371479 Sequence
41	107.2	5.8	2389	9 AF120278	AF120278 Homo sapi
42	107.2	5.8	2389	9 HSU82381	U82381 Human proli
43	106.8	5.8	2400	9 HSU79754	U79754 Human proli
44	105.8	5.8	2565	6 AX746760	AX746760 Sequence
45	105.8	5.8	2565	9 AK091063	AK091063 Homo sapi

ALIGNMENTS

RESULT 1

D83025 1833 bp mRNA PLN 06-FEB-1999

DEFINITION Arabidopsis thaliana mRNA for proline oxidase precursor, complete cds.

ACCESSION D83025

VERSION D83025.1 GI:1817543

KEYWORDS proline oxidase precursor; erds.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (sites) Kiyosue,T., Yoshida,Y., Yamaguchi-Shinozaki,K. and Shinozaki,K.

TITLE

A nuclear gene encoding mitochondrial proline dehydrogenase, an enzyme involved in proline metabolism, is upregulated by proline but downregulated by dehydration in Arabidopsis

JOURNAL

Plant Cell 8 (8), 1323-1335 (1996)

MEDLINE

96373198

PUBMED

8776899

REFERENCE

2 (bases 1 to 1833)
Kiyosue, T., Yoshida, Y., Yamaguchi-Shinozaki, Y. and Shinozaki, K.
Proline oxidase, the first enzyme involved in the conversion of proline to glutamate, in Arabidopsis thaliana: cDNA sequence, gene expression, immunological localization and functional complementation of yeast puti mutation

AUTHORS

Unpublished

TITLE

JOURNAL

Submitted (25-DEC-1995) Tomohiro Kiyosue, The Institute of Physical and Chemical Research (RIKEN), Tsukuba Life Science Center, Laboratory of Plant Molecular Biology; 3-1-1 Koyadai, Tsukuba, Ibaraki 305, Japan (E-mail: tkiyosue@rctcsl.riken.go.jp, Tel:81-298-36-4359, Fax:81-298-36-9060)

AUTHORS

Location/Qualifiers

JOURNAL

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1657. 1662

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1813. 1818

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1833

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ORIGIN

Query Match

Best Local Similarity

Matches 1833; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

polyA_signal

polyA_signal

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361 CACCCCGCTGTGATCGGCGCGCATATGCTCTATGCTCACTTGAAGAGTGGTAT 420

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541 AAGCGTTATGAGAGTACGCTCTTAAAGGAGTGTCTTATGCGCGTGAACACGCGCA 600

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661 ATCTTACCAACATCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

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VERSION	AY074571		
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana (chale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.		
AUTHORS	Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Banh,J., Bower,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamuya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.U., Quach,H.L., Sakurai,T., Saitou,M., Seki,M., Southwick,A., Tang,C.C., Tortum,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu.G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.		
TITLE	Arabidopsis cDNA clones		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1841)		
AUTHORS	Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Banh,J., Bower,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamuya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.U., Quach,H.L., Sakurai,T., Saitou,M., Seki,M., Southwick,A., Tang,C.C., Tortum,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu.G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-JAN-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,		
AUTHORS	USA		

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Natsumasa,M., Ishida,J., Satou,M., Kamuya,A., Sekurai,T., Carmichael,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shim,P., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Banb,J., Bowser,L., Chang,E., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,Y., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.D., Quach,H.L., Southwick,A., Tang,C.C., Tortum,M., Wu,H.C., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.

Shim,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

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 ORGANISM

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 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1854)

REFERENCE
 AUTHORS
 Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banth, J.,
 Bower, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
 Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G.,
 Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
 Narasaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,
 Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
 Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
 Davis, R.W., Theologis, A. and Ecker, J.R.
 Arabidopsis cDNA clones
 Unpublished
 2 (bases 1 to 1854)

TITLE
 JOURNAL
 Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banth, J.,
 Bower, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
 Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G.,
 Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
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 Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
 Davis, R.W., Theologis, A. and Ecker, J.R.
 Direct Submission
 Submitted (03-OCT-2001) Salk Institute Genomic Analysis Laboratory
 (SISAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA

COMMENT
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN
 Arabidopsis Full-Length cDNA'): Seki, M., Narasaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,

Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PSEC (SSP) Consortium members carried out the sequencing and annotation of the RFLV cDNAs: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Bahr, J., Bower, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Omodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Becker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Becker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

SOURCE

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 ORGANISM Arabidopsis thaliana
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 rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 1745)
 AUTHORS Peng, Z. and Verma, D.P.S.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-1996) Plant Biotechnology, Ohio State University,
 1060 Carmack Road, Columbus, OH 43210, USA
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 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE
 1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
 Katagiri, F., Quan, S., Tao, Y., Whitman, S., Xie, Z., Zhu, T. and Zou, G.
 TITLE Plant genes involved in defense against pathogens
 JOURNAL Patent: WO 03000898-A 362 03-JAN-2003;
 SynGene Participations AG (CH)

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DB	81081	CGAAACGTTAACCGCGGGAAGAAAGGAGCTCGAAAGCTCAGATGAGAAAGATTCA	81022	
QY	912	AAATCTGAGGAAATGCGCAGAGTCCATGATGATGATGATGATGATGATGATGAT	971	
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Db      481  TTCAACGAGCAAGACAGACCATCATTTACACACCATTCAGGCGTACTGAGAGAC 540
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      541  GCTGATGAGAGCTTCTGCTGCGCTTCAAGAGCCGAGAGAGAGAGTCTTCTAATGGT 600
Qy      1139  TTCAAGTTGATGAGAGGCGCTTACATGCTTACGCAAGCTAGCTTGGCGATTCCTGGGT 1198
      601  TTTAAGTTGATGAGAGGCGCTTATATGCTTACGCAAGCTATTCAGATTCCTGGGG 660
Qy      1199  TGCAGATC 1206
      661  CACAGATC 668
Db
RESULT 10
LOCUS   AB011478                      47460 bp    DNA    linear    PLN 27-DEC-2000
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, p1 clone:MKD10.
ACCESSION AB011478 BA000015
VERSION   AB011478.1 GI:2924655
KEYWORDS
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (sites)
AUTHORS  Kaneko, T., Kotani, H., Nakamura, Y., Sato, S., Asanizu, E., Miyajima, N.
          and Tabata, S.
TITLE    Structural analysis of Arabidopsis thaliana chromosome 5. V.
          Sequence features of the regions of 1,381,565 bp covered by twenty
          one physically assigned p1 and TAC clones
JOURNAL  DNA Res. 5 (2), 131-145 (1998)
MEDLINE  98344145
PUBMED   9679202
REFERENCE 2 (bases 1 to 47460)
AUTHORS  Nakamura, Y.
TITLE    Direct Submission
JOURNAL  Submitted (02-MAR-1998) Yasukazu Nakamura, Kazusa DNA Research
          Institute, Department of Plant Gene Research, 1532-3, Yana,
          Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,
          Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT  Address for correspondence: kaos@kazusa.or.jp
          For the latest information on annotation of this clone, please see
          http://www.kazusa.or.jp/kaos/cgi-bin/sgd_graph.cgi?c=MKD10
          Genes with similarity to proteins in the databases are described in
          'product' or 'note' qualifiers. Genes that have no significant
          protein similarity are described as 'unknown protein'.
          The software programs used to predict genes include: Grail
          (Informatics Group, Oak Ridge National Laboratory,
          http://compbio.ornl.gov/Grail-1.3/),
          GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
          NetGene2 (S.M. Hedsgaard, et al., CBS, Technical University of
          Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
          Solipeptide Predictor (Volker Brendel, Stanford University,
          http://gremml.zool.iastate.edu/cgi-bin/sp.cgi).
          Genes encoding tRNAs are predicted by tRNAscan-SE
          (Sean Eddy, Washington University School of Medicine, St. Louis,
          http://genome.wustl.edu/eddy/tRNAscan-SE/).
          This sequence may not be the entire insert of this clone. It may be
          shorter because we remove overlaps between neighboring submissions.
          The 5' clone is MB18 and the 3' clone is K156.
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Fax: 81-48-462-4674)

FEATURES

source

Location/Qualifiers

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/mol_type="mRNA"

/cultivar="Samsun NN"

/db_xref="taxon:4097"

1..1872

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/note="cyclokinin inducible gene in cultured green tobacco homolog of proline dehydrogenase/oxygenase"

/codon_start=1

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/protein_id="BAB83948.1"

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Best Local Similarity 59.8%; Pred. No. 1.2e-100; Mismatches 797; Conservative 0; Indels 9; Gaps 3;

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391 CTGTTACGGGTGTGCAACCTTAAGTGATGATGCAACGTGACATTCGAATGGCA 450

383 GCGATAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 442

451 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510

443 TCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 502

511 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 570

503 GCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 562

571 GCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627

563 CTTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622

628 TTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687

623 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 682

688 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747

683 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 742

748 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807

743 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 802

808 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 867

803 TTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 862

868 CTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 927

863 ACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 922

928 ACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987

923 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 982

988 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1047

983 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1042

1048 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104

1043 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1102

1105 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1164

1103 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1162

1165 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1224

1163 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1222

1225 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1284

1223 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1282

1285 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1344

1283 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342

1345 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1401

1343 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1402

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1403 CTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1462

1462 CTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1521

1463 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1522

1522 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1581

1523 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1582

1582 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1641

1583 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1642

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1702 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1714

RESULT 12

AK121010

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1

AK121010 1782 bp mRNA linear PLN 29-OCT-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J023047B13, full
insert sequence.
AK121010
AK121010.1 GI:37990633
FLI CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eubacillales; Oryzaceae; Oryza.

The Rice Full-length CDNA Consortium, National Institute of
Agricultural Sciences Rice Full-length CDNA Project Team,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Onsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Science 301 (5631), 376-379 (2003)

2

TITLE
JOURNAL
AUTHORS
REFERENCE
TITLE
JOURNAL

Unpublished

3 (bases 1 to 1782)

Kikuchi, S.

Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@niae.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 32k full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M. and Nakahama, Y.>

FAIS Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nakikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Taniguchi, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hara, A., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hori, F., Iida, J., Imamura, K., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa, Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohta, Y., Saitoh, H., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sato, K., Shibata, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K.,

Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takano-Akai, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

Location/Qualifiers

1. 1782

/organism="Oryza sativa (japonica cultivar-group)"

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/cultivar="Nipponbare"

/DB_xref="taxon:39947"

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Matches 694; Conservative 0; Mismatches 560; Indels 24; Gaps 6;

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407 ACGCGCGCTGAGTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 457
470 CTGTGAAAAGTACGTTTATGACATTTTGGCGCGGTGAAGATGCCAGCGCGCT 529
458 GCG 517
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635 GAGCG 691
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692 CTGTGCGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 751
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752 CCGCGCGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
830 CTCTACCAACAACCTCAAGACCGGAAACCGGTTAACCGCGGAAAGAGAGCTCGAA 889
812 CTGTACTGACG 871
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872 ATGCGCGACGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
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932 CTGTGACCGCGCGAGTACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 991
1010 GCGATCTGTTCAATGCTGCAAGAGCGCAACATGTTTCAACAGCATTCAGCGCTAC 1069
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RESULT 13

AF171226 333 bp mRNA linear PLN 11-AUG-1999
 LOCUS AF171226
 DEFINITION Brassica napus proline dehydrogenase (pdx) mRNA, partial cds.
 ACCESSION AF171226
 VERSION AF171226.1 GI:5726626
 KEYWORDS
 SOURCE
 ORGANISM Brassica napus (rape)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 333)
 Deleu, C., Nicogret, M.-F. and Larher, F.
 Isolation of a partial proline dehydrogenase cDNA from rape seed
 Unpublished
 2 (bases 1 to 333)
 Deleu, C., Nicogret, M.-F. and Larher, F.
 Direct Submision
 Submitted (23-JUL-1999) Physiologie et Biochimie Vegetales, CNRS
 UMR 6553, Avenue du General Leclerc, Rennes 35042, France
 JOURNAL
 TITLE
 AUTHORS
 REFERENCE
 JOURNAL
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ORIGIN

gene
 CDS
 ORIGIN

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 QY 1226 CAGGATCTCACTCTTGTTCATATGATGATTCCTGATGAGAAAGCATCAAC 1285
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 QY 1346 AGGAAAGCAGATGACCTCGGATGATTAACAGAACGGAAAGATGAGATTGACAGCTA 1405
 Db 181 AAGAAAGCAGATGACCTCAATGATGATTAAGAAAGGAGATGAGATTGACAGCTA 240
 QY 1406 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1465
 Db 241 TACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 1466 TACATGCCGTTTGAACCGGTCGAAACCGCTATA 1498
 Db 301 TACATGCCATTCGACCGGTCGAAACCGCTATA 333

RESULT 14

AX653926 1227 bp DNA linear PAT 22-MAR-2003
 LOCUS AX653926
 DEFINITION Sequence 3796 from Patent WO03000898.
 ACCESSION AX653926
 VERSION AX653926.1 GI:29156740
 KEYWORDS
 SOURCE
 ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
 Katagiri, F., Quan, S., Tao, Y., Whitman, S., Xie, Z., Zhu, T. and Zou, G.
 TITLE Plant genes involved in defense against pathogens
 JOURNAL Patent: WO 03000898-A 3796 03-JAN-2003;
 Syngenta Participations AG (CH)
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ORIGIN

Query Match 14.1%; Score 258; DB 6; Length 1227;
 Best Local Similarity 55.3%; Pred. No. 4.4e-54;
 Matches 583; Conservative 2; Mismatches 457; Indels 12; Gaps 4;

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 QY 629 CAACATTCATTCGACATTCGACATTCGACATTCGACATTCGACATTCGACATTCGACATTC 688
 Db 67 GCGGATCTTGTCTATGGCGCTGCAACAGCGCGGAGAGCGCGCGCTGCGACCGCAACGCGC 123
 QY 689 GTGCTTGTGAAGTAACTGCAATTTGTCCAAATTAATCTTCTTGAAGAGAGTGAAGCATG 748
 Db 124 GTGCTGATCAAGATCAAGCGCGCTGCGCGGCTGCTGCAAGAGCGGAGTAACTG 183
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Thu Mar 11 07:51:07 2004

us-10-026-767-3.rge

Page 19

Search completed: March 10, 2004, 19:22:16
Job time : 6892.99 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: March 10, 2004, 09:18:05 ; Search time 628.751 Seconds
(without alignments)
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Title: US-10-026-767-3

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 30	107.2	5.8	1551	9	ADB38902	ADB38902 Human pro
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ALIGNMENTS

RESULT 1

ID ABX93779 standard; CDNA; 1833 BP.

AC ABX93779;

DT 17-JUN-2003 (first entry)

DE Thale cress proline dehydrogenase (ProDH) antisense cDNA.

XX Grass: delta¹-pyrroline-5-carboxylate synthetase; P5CS; gene; ss;

KW proline dehydrogenase; ProDH; stress tolerance; water tolerance; calli;

KM salt stress; salinity tolerance; temperature tolerance; protoplast;

KW proline accumulation; thale cress; antisense.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

PN GB2376236-A.

XX 11-DEC-2002.

PD 24-DEC-2001; 2001GB-00030946.

PF 08-JUN-2001; 2001JP-00174553.

XX (HITA) HITACHI LTD.

PA (BIO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

PA (INDE-) INDEPENDENT ADMINISTRATIVE INST NAT INST.

XX (RIKE) RIKEN KK.

XX Yoshida Y, Shinozaki K;

XX WPI; 2003-203644/20.

XX P-PSDB; ABU09031.

XX New grass plant overexpressing a P5CS gene from rice, useful for making

XX transgenic plants with higher levels of proline accumulating ability, and

XX more improved salinity-tolerance, drought-tolerance and low temperature-

XX tolerance.

XX Claim 3; Page 37-42; 52pp; English.

XX The invention relates to a grass plant in which a delta¹-pyrroline-5-carboxylate synthetase (P5CS) gene of rice, or a P5CS gene of Arabidopsis thaliana and the antisense gene of a proline dehydrogenase (P5DH) gene of Arabidopsis thaliana, have been introduced in tandemly connected relation to each other. A new method of the present invention is useful for the production of a transgenic rice plant with improved stress tolerance, especially for water or salt stress and low temperatures. The invention provides for transgenic plants with a higher level of proline accumulating ability. The invention also relates to a grass plant obtained by introducing a vector comprising a gene of the invention into a calli or protoplast derived from a grass plant, growing the calli or protoplast to obtain a colony and regenerating a plant body from the calli or colony. This sequence represents DNA encoding the thale cress ProDH polypeptide of the invention

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Query Match 100.0%; Score 1833; DB 7; Length 1833;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 18-OCT-2000 (first entry)
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KW protein identification; signal transduction pathway; metabolic pathway;
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 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 96.5%; Score 1769.2; DB 3; Length 1835;

Best Local Similarity 98.5%; Pred. No. 0; Mismatches 23; Indels 4; Gaps 1;

Matches 1797; Conservative 0;

QY 5 TTTGAAAAAAGCGCATTAACCGAAGCATCAAGCAACAAAAAAGAGAGAGAG 64
 DB 16 TTAGAAAAAAGCGCATTAACCGAAGCATCAAGCAACAAAAAAGAGAGAGAG 71
 QY 65 AATTATTTTTTTTGTGTTTGTGTTTCAAAAAAATCTTGAATTTTATGCGAACCCGT 124
 DB 72 AATTATTTTTTTTGTGTTTGTGTTTCAAAAAAATCTTGAATTTTATGCGAACCCGT 131
 QY 125 CTTCGCGAAGAACTTATCCGCGGATCTTACCGGTTTACCGCGGTGGGT 184
 DB 132 CTTCGCGAAGAACTTATCCGCGGATCTTACCGGTTTACCGCGGTGGGT 191

QY 185 CTTCCACCGTGAATGCTTCCACCGCGCTGTCGCCGAGATTTCTCTTTGAGACAA 244
 DB 192 CTTCCACCGTGAATGCTTCCACCGCGCTGTCGCCGAGATTTCTCTTTGAGACAA 251
 QY 245 GCACCGGAACCACTCTTTTCAACCAACCAACCAACCAACCAACCAACCAACCA 304
 DB 252 GCACCGGAACCACTCTTTTCAACCAACCAACCAACCAACCAACCAACCAACCA 311
 QY 305 CTCTCCGATTAACCGCGTCTTTCTCTCTATCCGACCTGATCTCTCTCTCTCT 364
 DB 312 CTCTCCGATTAACCGCGTCTTTCTCTCTATCCGACCTGATCTCTCTCTCTCT 371
 QY 365 GCCGTGTCATGCGCGGCGATAGGTCTTATGTCGATGAGAGAGAGAGAGAGAG 424
 DB 372 GCCGTGTCATGCGCGGCGATAGGTCTTATGTCGATGAGAGAGAGAGAGAGAG 431
 QY 425 TCTTAATTTATGACGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
 DB 432 TCTTAATTTATGACGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
 QY 485 TTTTATGACCAATTTTTCGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
 DB 492 TTTTATGACCAATTTTTCGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
 QY 545 GTTTATGAGTACTGCTCTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
 DB 552 GTTTATGAGTACTGCTCTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 611
 QY 605 GCTGTATCTGTGATGATTAATGATCAATCAATCAATCAATCAATCAATCAATCA 664
 DB 612 GCTGTATCTGTGATGATTAATGATCAATCAATCAATCAATCAATCAATCAATCA 671
 QY 665 TTACCAATCTCACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 724
 DB 672 TTACCAATCTCACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 731
 QY 725 CTTCGAAAG 784
 DB 732 CTTCGAAAG 791
 QY 785 TCAATGAGAGTCAATGCTTCCGCTTTTCCGATGATGATGATGATGATGATGATGAT 844
 DB 792 TCAATGAGAGTCAATGCTTCCGCTTTTCCGATGATGATGATGATGATGATGATGAT 851
 QY 845 TCAAGACCGAAGCGTTAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
 DB 852 TCAAGACCGAAGCGTTAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911
 QY 905 ATTCAAGAAATCTGTAGAGAAATGCAAGAGTCAATGATGATGATGATGATGATGAT 964
 DB 912 ATTCAAGAAATCTGTAGAGAAATGCAAGAGTCAATGATGATGATGATGATGATGAT 971
 QY 965 GACCAATCTCCCAACCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1024
 DB 972 GACCAATCTCCCAACCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1031
 QY 1025 GCTGCAAGACCGAAGCAATGTTTCAACCAAGTCAAGCGGATCTTGAAGAGAGAG 1084
 DB 1032 GCTGCAAGACCGAAGCAATGTTTCAACCAAGTCAAGCGGATCTTGAAGAGAGAG 1091
 QY 1085 GAGAGATCTGATTTGAGAGTCAAAATGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1144
 DB 1092 GAGAGATCTGATTTGAGAGTCAAAATGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1151
 QY 1145 TTGCTGAGAGGAGCTTATCATGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1204
 DB 1152 TTGCTGAGAGGAGCTTATCATGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1211
 QY 1205 TCGCAGTTCACAGACAAATCAAGATCTCACTCTTCAATGATGATGATGATGATGAT 1264
 DB 1212 TCGCAGTTCACAGACAAATCAAGATCTCACTCTTCAATGATGATGATGATGATGAT 1271

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 PR 26-AUG-1999; 99US-0150884P.
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 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
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 PR 29-SEP-1999; 99US-0156596P.
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 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 96.3%; Score 1764.8; DB 3; Length 1844;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1803; Conservative 0; Mismatches 22; Indels 5; Gaps 2;

5 TTTGAAAAAAGCGATTAACCGAATCAAGCAAAAGAGAGA 64
 16 TTGAAAAAAGCGATTAACCGAATCAAGCAAAAGAGAGA 71
 65 AATTATTTTGTGTTTGTGTTTCAAAAAGAAATTTGAATTTATGCAACCGT 124
 72 AATTTTGTGTTTGTGTTTGTGTTTCAAAAAGAAATTTGAATTTATGCAACCGT 131
 125 CTTCTCCGAACAACTTTATCCGCGCATCTTACCGTTTACCGCTTTAGCCGGTGGT 184
 132 CTTCTCCGAACAACTTTATCCGCGCATCTTACCGTTTACCGCTTTTACCGGGTGGT 191
 185 CTTCCACCGGATGCTGCTTCACCGCGCGTGTCCGGAAGTTCTCTCTTTGACAA 244
 192 CTTCCACCGGATGCTGCTTCACCGCGCGTGTCCGGAAGTTCTCTCTTTGACAA 251
 245 GCACCGGACCACTCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 304
 252 GCACCGGACCACTCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 311
 305 CTTCCGATCAAGCCGCTTTCTCTATCCCACTCTGATCTCTCCGTTCCACC 364
 312 CTTCCGATCAAGCCGCTTTCTCTATCCCACTCTGATCTCTCCGTTCCACC 371
 365 GCCGTTGATGCGCGCGCGGATGCTCTATGTCACCTAGGAGAGTGGTCTATAGC 424
 372 GCCGTTGATGCGCGCGCGGATGCTCTATGTCACCTAGGAGAGTGGTCTATAGC 431
 425 TCTAACTTATGACGCTGCTGATGACCGGTGCAATGTTTATGAGCTTGTGAAGTACG 484
 432 TCTAACTTATGACGCTGCTGATGACCGGTGCAATGTTTATGAGCTTGTGAAGTACG 491
 485 TTTTATGACATTTTGGCGCGGATGAAAGATCCGACGACCGGTGAGCGGTGAGAAC 544
 492 TTTTATGACATTTTGGCGCGGATGAAAGATCCGACGACCGGTGAGCGGTGAGAAC 551
 545 GTTTATGACATCTGCTTAAAGGATGCTTATGAGCGGTGAGCGGTGAGAAC 604
 552 GTTTATGACATCTGCTTAAAGGATGCTTATGAGCGGTGAGCGGTGAGAAC 611
 605 GCTGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
 612 GCTGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671

QY 665 TTACCAACATCTCACTTTAGTCTCAGTGGTGTGAAGATAAAGTCCATTTGTCCTCAATAGT 724
Db 672 TTACCAACATCTCACTTTAGTCTCAGTGGTGTGAAGATAAAGTCCATTTGTCCTCAATAGT 731
QY 725 CTTCTGAAACGAGTGAAGGATCTCTGCTGGTGGGAATACAAAAGTCCGAATCTCAAACTC 784
Db 732 CTTCTGAAACGAGTGAAGGATCTCTGCTGGTGGGAATACAAAAGTCCGAATCTCAAACTC 791
QY 785 TCATGGAAGCTCAAAATCGTTTCCGGTTTCTCCGAATCGAGTCTCTCTACCAACACAAAC 844
Db 792 TCATGGAAGCTCAAAATCGTTTCCGGTTTCTCCGAATCGAGTCTCTCTACCAACACAAAC 851
QY 845 TCAGAACCGGAACCGTTAAACCGCGGAAGAAAGAGGAGCTCGAAGCAGCTCATGGAAG 904
Db 852 TCAGAACCGGAACCGTTAAACCGCGGAAGAAAGAGGAGCTCGAAGCAGCTCATGGAAG 911
QY 905 ATTCAGGAATCTGAGGAATGCC-AAGAGTCCAATGTACCATTTGTTGATGATCGGA 963
Db 912 ATTCAGGAATCTGAGGAATGCCAAGAGTCCAATGTACCATTTGTTGATGATCGGA 971
QY 964 AGACACATCTCCAAACCGCGATCGATTACATGGCTTATTCATCGCGATCATGTTCAA 1023
Db 972 AGACACATCTCCAAACCGCGATCGATTACATGGCTTATTCATCGCGATCATGTTCAA 1031
QY 1024 TGCTGACAAAGACCGAACCAATCGTTTACACACAGTTCAGCGTACTTGAGAGCGCGG 1083
Db 1032 TGCTGACAAAGACCGAACCAATCGTTTACACACAGTTCAGCGTACTTGAGAGCGCGG 1091
QY 1094 TGAGAGACTGCATTTGGCAGTACAAAATGCTGAGAAAGAGAAATGCTTATGGGTTCAA 1143
Db 1092 TGAGAGACTGCATTTGGCAGTACAAAATGCTGAGAAAGAGAAATGCTTATGGGTTCAA 1151
QY 1144 GTTGTGAGAGGGCTTACATGCTAGCGAACGTAGCTTGGCGGATTCCTCTGGTTGCAA 1203
Db 1152 GTTGTGAGAGGGCTTACATGCTAGCGAACGTAGCTTGGCGGATTCCTCTGGTTGCAA 1211
QY 1204 GTCCGAGTCCACGACACAAATTCAGGATPACTCTTTGTGTAATGATGATGACAT 1263
Db 1212 GTCCGAGTCCACGACACAAATTCAGGATPACTCTTTGTGTAATGATGATGACAT 1271
QY 1264 CCTGATGAGAAAGCATCAACCGTTCTGGTTTGGTGTGCTTCGCAACACATAACGC 1323
Db 1272 CCTGATGAGAAAGCATCAACCGTTCTGGTTTGGTGTGCTTCGCAACACATAACGC 1331
QY 1324 TGATTCGGGGAGACTTGGCTCGAGAAAGCAGTGAAGCTCGGGATCGATAAAGACGAG 1383
Db 1332 TGATTCGGGGAGACTTGGCTCGAGAAAGCAGTGAAGCTCGGGATCGATAAAGACGAG 1391
QY 1384 GAAGATAGAGTTTGACAGCTATATGGTATGTCAGATGCTATGTCCTTCGGGTTAAAGAG 1443
Db 1392 GAAGATAGAGTTTGACAGCTATATGGTATGTCAGATGCTATGTCCTTCGGGTTAAAGAG 1451
QY 1444 AGCAGGTTCAATGTTAGCAAGTACATCCGTTTGGACCGTTCGCAACCGTATACCGTA 1503
Db 1452 AGCAGGTTCAATGTTAGCAAGTACATCCGTTTGGACCGTTCGCAACCGTATACCGTA 1511
QY 1504 TCTTCTCCGACGCTTATGAGAACCGGGGATGATGCGCCAGCTCATGACCGTCA 1563
Db 1512 TCTTCTCCGACGCTTATGAGAACCGGGGATGATGCGCCAGCTCATGACCGTCA 1571
QY 1564 ACTCATAGGATGGAACCTTAAGAGAGATTAATCGCCGGGATTCGTAAGAGAGAGAT 1623
Db 1572 ACTCATAGGATGGAACCTTAAGAGAGATTAATCGCCGGGATTCGTAAGAGAGAGAT 1631
QY 1624 GGAGCCATTAAATGAATGGGAATGAGATGAATTAATTTCTTCTATGATGATTAAGA 1683
Db 1632 GGAGCCATTAAATGAATGGGAATGAGATGAATTAATTTCTTCTATGATGATTAAGA 1691
QY 1684 AATTGAAACAAAAATTAATAAAGAAATGAGTGGTAAAGACATTTCTGTGGCT 1743
Db 1692 AATTGAAACAAAAATTAATAAAGAAATGAGTGGTAAAGACATTTCTGTGGCT 1751
QY 1744 AATATTTTTCATGAGGAGCTATGTTTCTATCTATCATATATATCATACAAATGTATTT 1803

Db 1752 AATATTTTTCATGAGGAGCTATGTTTCTATCTATCATATATATCATACAAATGTATTT 1811
QY 1804 CACCTTATCAATAAAATGCTTTTACTTTT 1833
Db 1812 CACCTTATCAATAAAATGCTTTTACTTTT 1841
RESULT 4
AAC42169
ID AAC42169 standard; DNA; 1837 BP.
XX AAC42169;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34546.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
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PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 13-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 29-SEP-1999; 99US-0157117P.
PR 04-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.

Db 1621 TTACTATCAATATATCATTCACAAATGTATATTCACCTTATCAATAAATGCTTTTAA 1680
QY 1630 CTTT 1633
Db 1681 CTTT 1684

RESULT 6
ADA68100
ID ADA68100 standard; DNA; 1500 BP.

XX ADA68100;
AC-
XX 20-NOV-2003 (first entry)
XX
XX Arabidopsis thaliana gene, SEQ ID 362.
DE
XX Arabidopsis thaliana infection; fungal infection; viral infection; ds.
XX
XX Plant; bacterial infection; fungal infection; viral infection; ds.
XX
XX Arabidopsis thaliana.
XX
XX WO2003000898-A1.
XX
XX 03-JAN-2003.
XX
XX 22-JUN-2001; 2001WO-1B001105.
XX
XX 22-JUN-2001; 2001WO-1B001105.
XX
XX 22-JUN-2001; 2001WO-1B001105.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
PI Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G,
XX
XX MPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 6; SEQ ID NO 362; 899bp; English.

CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX
XX Sequence 1500 BP; 383 A; 374 C; 371 G; 372 T; 0 U; 0 Other;

QY Query Match 81.3%; Score 1490.4; DB 7; Length 1500;
Db Best Local Similarity 99.6%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 113 ATGGCAACCCGCTCTTCCTCGAACAACCTTTATCCGGCGATCTTACCGTTTACCCGCTTTT 172
Db 1 ATGGCAACCCGCTCTTCCTCGAACAACCTTTATCCGGCGATCTTACCGTTTACCCGCTTTT 60

QY 173 AGCCCGGTGGGTCTCCCAACCGTGAACGCTTCACACCGCGTGTCCCGAGATTCCTCC 232
Db 61 AGCCCGGTGGGTCTCCCAACCGTGAACGCTTCCTCCACCGCGCTGTCCCGAGATTCCTCC 120

QY 233 TTGTGACAAACGACCGGACCAACCTCTTACACACCCAAACCCACCGAGCAATCTCAC 292
Db 121 TTGTGACAAACGACCGGACCAACCTCTTACACACCCAAACCCACCGAGCAATCTCAC 180

QY 293 GATGGTCTGATCTCTCCGATCAAGCCCGTCTTTCTCTCTATCCCAACCTCTGATCTC 352

Db 181 GATGGTCTGATCTCTCCGATCAAGCCCGTCTTTCTCTCTATCCCAACCTCTGATCTC 240
QY 353 CTCCGTTCCACCGCCGCTGTGCAATGGCGGCGGATAGTCTCTATGGTCAACCTAGGAGAG 412
Db 241 CTCCGTTCCACCGCCGCTGTGCAATGGCGGCGGATAGTCTCTATGGTCAACCTAGGAGAG 300

QY 413 TGGGTCAATGAGCTCTAACTTAATGAGACGCTTCGATGACGCGTGGCAATGTTTTAGGAGCTT 472
Db 301 TGGGTCAATGAGCTCTAACTTAATGAGACGCTTCGATGACGCGTGGCAATGTTTTAGGAGCTT 360

QY 473 GTGAAAAGTACGTTTATGACCAATTTTGGCCGCTGAAAGATTCGCAACGAGCCGCTGAG 532
Db 361 GTGAAAAGTACGTTTATGACCAATTTTGGCCGCTGAAAGATTCGCAACGAGCCGCTGAG 420

QY 533 CGCGTGAAGACGCTTATGAGACTACGTGCTTAAAGGATGCTTCTATGCGCTGAA 592
Db 421 CGCGTGAAGACGCTTATGAGACTACGTGCTTAAAGGATGCTTCTATGCGCTGAA 480

QY 593 CACGCGATGACGCTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 652
Db 481 CACGCGATGACGCTGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

QY 653 GCTGCCAAATCTTATCAACATCATCTTATGCTCACTGCTGCTGCTGCTGCTGCTGCTGCT 712
Db 541 GCTGCCAAATCTTATCAACATCATCTTATGCTCACTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 713 TGTCCAAATGATCTTCTGAAACGATGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772
Db 601 TGTCCAAATGATCTTCTGAAACGATGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 773 AACTTCAAACTCTCTATGAGAGCTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832
Db 661 AACTTCAAACTCTCTATGAGAGCTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

QY 833 TACCAACAACCTCAAGACCGGAAACGCTTAAACCGCGGAGAGAGAGAGAGAGAGAGAGAG 892
Db 721 TACCAACAACCTCAAGACCGGAAACGCTTAAACCGCGGAGAGAGAGAGAGAGAGAGAGAG 780

QY 893 GCTCATGAAAGATTCAGAAATCTGTGAGAAATGCCAAGATTCATGATGATGATGATGAT 952
Db 781 GCTCATGAAAGATTCAGAAATCTGTGAGAAATGCCAAGATTCATGATGATGATGATGAT 840

QY 953 ATTGATGGGAGAGCAACATCTCTCAACCGCGATGATGATGATGATGATGATGATGATGAT 1012
Db 841 ATTGATGGGAGAGCAACATCTCTCAACCGCGATGATGATGATGATGATGATGATGATGAT 900

QY 1013 ATCATGTTCAATGCTGACAAAGACCGCAACATGCTTTTACACACGATTCAGCGCTACTTG 1072
Db 901 ATCATGTTCAATGCTGACAAAGACCGCAACATGCTTTTACACACGATTCAGCGCTACTTG 960

QY 1073 AGAAGCCCGGTGAGACATGCAATTTGGCGATGCAAAATGCTGAGAAAGAGATGTTCTT 1132
Db 961 AGAAGCCCGGTGAGACATGCAATTTGGCGATGCAAAATGCTGAGAAAGAGATGTTCTT 1020

QY 1133 ATGGGTTTCAAGTTGTGAGAGGGGCTTACATGCTAGCGAACGTAGCTTGGCGATTTCC 1192
Db 1021 ATGGGTTTCAAGTTGTGAGAGGGGCTTACATGCTAGCGAACGTAGCTTGGCGATTTCC 1080

QY 1193 CTGGGTTGCAAGTGCACAGTCCAGACACAAATTCAGATCTCACTTGTTCATGATGAT 1252
Db 1081 CTGGGTTGCAAGTGCACAGTCCAGACACAAATTCAGATCTCACTTGTTCATGATGAT 1140

QY 1253 TGTATGACATTCCTGATGAGAGAAAGCATCAACGCTTCTGCTTCTGCTGCTGCTGCTGCA 1312
Db 1141 TGTATGACATTCCTGATGAGAGAAAGCATCAACGCTTCTGCTTCTGCTGCTGCTGCTGCA 1200

QY 1313 ACAATTAACGTTGATTTGGGGAGACTTGGCTCAGAGAAACCGATGATCTCCGAGATGAT 1372
Db 1201 ACAATTAACGTTGATTTGGGGAGACTTGGCTCAGAGAAACCGATGATCTCCGAGATGAT 1260

QY 1373 AAACAGAAACGAGATGATGATTTGCAACAGCTATATGATGATGATGATGATGATGATGAT 1432

QY 1292 GATTGCGTGTCTTCTCGCAACATTAAGCTGATTGCGGGAGACTTGCCTGCGAGAA 1351
 DB 1141 GATTGCGTGTCTTCTCGCAACATTAAGCTGATTGCGGGAGACTTGCCTGCGAGAA 1200
 QY 1352 GCGAGTGAAGCTGCGGATTCATTAACGAAACGGAAGATGAGTTGGACAGCTATATG 1411
 DB 1201 GCGAGTGAAGCTGCGGATTCATTAACGAAACGGAAGATGAGTTGGACAGCTATATG 1260
 QY 1412 ATGTGAGATGATTCCTTCTCGCAACATTAAGCTGATTGCGGGAGACTTGCCTGCGAGAA 1471
 DB 1261 ATGTGAGATGATTCCTTCTCGCAACATTAAGCTGATTGCGGGAGACTTGCCTGCGAGAA 1320
 QY 1472 CCGTTTGAACCCGCTGCAACCGCTATACCGTATCTTCTCGCAACCGCTTATGAAACCGG 1531
 DB 1321 CCGTTTGAACCCGCTGCAACCGCTATACCGTATCTTCTCGCAACCGCTTATGAAACCGG 1380
 QY 1532 GGAATATGGCCACCGGAGCTCATGACGCTCACTCATGAGATGGAATTAAGAGAGA 1591
 DB 1381 GGAATATGGCCACCGGAGCTCATGACGCTCACTCATGAGATGGAATTAAGAGAGA 1440
 QY 1592 TTAATGCGCGGATTCGCTTA 1612
 DB 1441 TTAATGCGCGGATTCGCTTA 1461

RESULT 8
 AEN98243 standard; DNA; 1339 BP.
 ID AEN98243; standard; DNA; 1339 BP.
 AC AEN98243; standard; DNA; 1339 BP.
 XX AEN98243; standard; DNA; 1339 BP.
 DT 01-AUG-2002 (first entry)
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 11.
 XX Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
 KM disease; crop; thale cress; tolerance factor; insect; pathogen;
 XX nutrition; ds.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX US2002023281-A1.
 PN US2002023281-A1.
 XX 21-FEB-2002.
 PD 21-FEB-2002.
 XX 26-JAN-2001; 2001US-00770445.
 PF 26-JAN-2001; 2001US-00770445.
 XX 27-JAN-2000; 2000US-0178472P.
 PR 27-JAN-2000; 2000US-0178472P.
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAM/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (MOES/) MOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICK/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX GORLACH J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Moessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N,
 PI Hurban P;

XX WPI: 2002-403163/43.
 DR New Arabidopsis thaliana nucleic acid for identifying homologous genes,
 XX producing compositions that modulate the expression or function of its
 PT encoded protein, and mapping functional regions of protein.
 PS Claim 1; SEQ ID NO 11; 49pp + Sequence Listing; English.

XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
 CC comprising a sequence capable of hybridizing under stringent conditions
 CC to a sequence selected from any one of 999 sequences (AEN98243-AEN99231),
 CC given in the specification or its fragment. A polypeptide (II) encoded by
 CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
 CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
 CC useful for screening a candidate agent for its biological effect. (I) is
 CC useful in identifying homologous or related genes, in producing
 CC compositions that modulate the expression or function of its encoded
 CC protein, mapping functional regions of the protein and in studying
 CC associated physiological pathways. (I) is also useful for the genetic
 CC manipulation of cells, particularly plant cells. (I) is also useful in
 CC screening assays of various plant strains to determine the strains that
 CC are best capable of withstanding a particular disease or environmental
 CC stress. (II) and (III) are useful for screening of biologically active
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
 CC pathways. The screened agents are useful in improved methods of treating
 CC crops to prevent or treat disease. (II) are also useful in screening
 CC programs to identify agents that mimic or enhance the action of tolerance
 CC factors. Such agents are useful in improved methods of treating crops to
 CC enhance their tolerance to environmental stress. (I) is also useful for
 CC enhancing or inhibiting production of a biosynthetic product in a plant.
 CC (III) is useful for identifying other mediators that may induce
 CC expression of proteins of interest, for establishing the extent to which
 CC any specific insect and/or pathogen is responsible for damage to a
 CC particular plant, for identifying other mediators that enhance or induce
 CC tolerance to environmental stress, for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial, or medicinal value and
 CC for identifying productions of nutritional, commercial or medicinal
 CC value. (IV) is useful in the study of genetic function and regulation,
 CC for alteration of the cellular metabolism and for screening compounds
 CC that may affect the biological function of the gene or gene products.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=99909770445

XX Sequence 1339 BP; 360 A; 280 C; 352 G; 327 T; 0 U; 20 Other;
 SQ

Query Match 69.9%; Score 1280.6; DB 6; Length 1339;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 1295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 351 TCTCCGTTCCACCGCGGTGTCATGCGCGGCAATAGTCTTATGTCGACTTGGGA 410
 DB 1 TCGAGCGCGCGCGCGGAGTCATGCGCGGCAATAGTCTTATGTCGACTTGGGA 60
 QY 411 CGTGGGTCATGAGCTCTAACTTATGAGCGCTTCCGTGACGCGTGCATGTTTGGGC 470
 DB 61 CGTGGGTCATGAGCTCTAACTTATGAGCGCTTCCGTGACGCGTGCATGTTTGGGC 120
 QY 471 TTGTGAAGATGAGTTTATGACCAATTTTGGCCGCGTGAAGATGCCAGCGCGCTG 530
 DB 121 TTGTGAAGATGAGTTTATGACCAATTTTGGCCGCGTGAAGATGCCAGCGCGCTG 180
 QY 531 AGCGCGTGAAGAGTTTATGAGCTATGCTTAAAGGATGCTTGTATGAGCGTGC 590
 DB 181 AGCGCGTGAAGAGCTTTATGAGGCTTAAAGGATGCTTGTATGAGCGTGC 240
 QY 591 AACACGCGATGACGCTGATCTTGTGATGATTAACGACCAATTCATTGGAACATTG 650
 DB 241 AACACGCGATGACGCTGATCTTGTGATGATTAACGACCAATTCATTGGAACATTG 300
 QY 651 AAGGTGCAATCTTTTACCAATCTCACTTGTGCTGAGGTGTTGAAGATTAACGCA 710

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Db 301 AAGTCGCAAACTTTTACCAACATCTCACTTAGCTCAGTGTGTGAGATACTCCCA 360
Qy 711 TTTGTCCATTAGTCTTCTGAAAAGAGTGAAGCATCTGCTGCGGTGGGAATCAAAAGTC 770
Db 361 TTTGTCCATTAGTCTTCTGAAAAGAGTGAAGCATCTGCTGCGGTGGGAATCAAAAGTC 420
Qy 771 CGAAGCTCAAACTCTCATGGAAGTCAAAATGTTTCCGTTTCTCCGAATCGAGTCTC 830
Db 421 CAAGCTCAAACTCTCATGGAAGTCAAAATGTTTCCGTTTCTCCGAATCGAGTCTC 480
Qy 831 TCTACACACAACTCTCAAGACCGGAACTGTTAACCGGGAAGAAAGAGAGTCTGAAG 890
Db 481 TCTACACACAACTCTCAAGACCGGAACTGTTAACCGGGAAGAAAGAGAGTCTGAAG 540
Qy 891 CAGCTCATGGAAGATTCAGAAATCTGTAGAAATGCAAGATGCAATGTCATTTGT 950
Db 541 CAGCTCATGGAAGATTCAGAAATCTGTAGAAATGCAAGATGTCATTTGT 600
Qy 951 TGATTGATGCGGAAGACAAATCTCCAAACCCGGAATGATTACATGCTTATTCATCGG 1010
Db 601 TGATTGATGCGGAAGACAAATCTCCAAACCCGGAATGATTACATGCTTATTCATCGG 660
Qy 1011 CGATCATGTTCAATGCTGACAAAGACGACCAATGTTTCAACAGATTCAGGCGTACT 1070
Db 661 CGATCATGTTCAATGCTGACAAAGACGACCAATGTTTCAACAGATTCAGGCGTACT 720
Qy 1071 TGAGAGACGCGGTGAGAGATGCAATTTGCGATGACAAATGCTGAGAAAGAGATTTTC 1130
Db 721 TGAGAGACGCGGTGAGAGATGCAATTTGCGATGACAAATGCTGAGAAAGAGATTTTC 780
Qy 1131 CTATGCGGTCTCAAGTTGTGTGAGAGGGGCTTACATGTTAGCGAAAGTACTTGGCGATT 1190
Db 781 CTATGCGGTCTCAAGTTGTGTGAGAGGGGCTTACATGTTAGCGAAAGTACTTGGCGATT 840
Qy 1191 CCGTGGGTTGCAAGTCGCGAGTCCACGACCAATTCAGATCTCAGTCTTTGTTACATG 1250
Db 841 CCGTGGGTTGCAAGTCGCGAGTCCACGACCAATTCAGATCTCAGTCTTTGTTACATG 900
Qy 1251 ATTGTATGACATTCCTGATGAGAGAAAGCATCAACGGTCTGCTGCTGCTGCTGCTG 1310
Db 901 ATTGTATGACATTCCTGATGAGAGAAAGCATCAACGGTCTGCTGCTGCTGCTGCTG 960
Qy 1311 CAACCATTAAGCTGATTCGGGGGAGACTTGTGTGAGAGAAAGAGTGAAGTGGGGATG 1370
Db 961 CAACCATTAAGCTGATTCGGGGGAGACTTGTGTGAGAGAAAGAGTGAAGTGGGGATG 1020
Qy 1371 ATAAACAGAACGGAAGATAGATTGTCACAGCTATATGATGTCAAGTATGTCCT 1430
Db 1021 ATAAACAGAACGGAAGATAGATTGTCACAGCTATATGATGTCAAGTATGTCCT 1080
Qy 1431 TCGGGTTAAAGAGAGAGGTTCAATGTTAGCAAGTATGATCCGTTGGACCCGTCGCA 1490
Db 1081 NCGANNNTNNAAGACANNNNNNNATGTNAGCAAGTATGATNNNTTGGACCCGTCGCA 1140
Qy 1491 CCGCTATACCGTATCTTCCGACGCGCTTATGAGAACCGGGGAATGATGCGCACCGGAG 1550
Db 1141 CCGCTATACCGTATCTTCCGACGCGCTTATGAGAACCGGGGAATGATGCGCACCGGAG 1200
Qy 1551 CTCATGACCGTCACTCATGAGATGAACTTTAAGAGAGATTAATGCGCGGATTCGCT 1610
Db 1201 CTCATGACCGTCACTCATGAGATGAACTTTAAGAGAGATTAATGCGCGGATTCGCT 1260
Qy 1611 AAAGAGAGATGAGGACATTAATGAAATTTGGGAAATGTAGATGAAATTTCTCT 1670
Db 1261 AAAGAGAGATGAGGACATTAATGAAATTTGGGAAATGTAGATGAAATTTCTCT 1320
Qy 1671 ATGTAGTTTAAAGAAATGA 1689
Db 1321 ATGTAGTTTAAAGAAATGA 1339

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RESULT 9
AAFB7062

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ID AAFB7062 standard; DNA; 1850 BP.
XX
AC AAFB7062;
XX
DT 09-OCT-2001 (first entry)
XX
DE M. sativa Pdh gene.
XX
KW pdh gene; proline dehydrogenase; alfalfa; transgenic plant; drought;
XX proline level; environmental stress; high salinity; temperature; ds.
XX
OS Medicago sativa.
XX
FH Key Location/Qualifiers
FT CDS 106..1581
FT /tag= a
FT /product= "Pdh"
FT /note= "Proline dehydrogenase"
XX
XX MO200153323-A2.
XX
XX 26-JUL-2001.
XX
XX 10-JAN-2001; 2001MO-IL000026.
XX
XX PR 24-JAN-2000; 2000US-00490454.
XX
XX PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX (AGRI-) AGRIC RES ORG VOLCANI CENT.
XX
XX Stein H, Zilberstein A, Miller G, Kapulnik Y;
XX
XX MPI; 2001-483133/52.
XX P-PSDB; AAB83319.
XX
XX Novel isolated nucleic acid used to create transgenic plants with
XX increased proline levels and resistance to environmental stress e.g. high
XX PT salinity, drought.
XX
XX Claim 4; Page 95-96; 99pp; English.
XX
XX This sequence encodes the Medicago sativa (alfalfa) proline dehydrogenase
XX (Pdh) of the invention. The Pdh gene is used to create transgenic plants
XX with increased proline levels and which is therefore resistant to
XX environmental stress. Environmental stress conditions are high salinity,
XX extreme temperature or drought.
XX
XX Sequence 1850 BP; 561 A; 352 C; 389 G; 548 T; 0 U; 0 Other;
XX
XX
XX Query Match 25.9%; Score 474.8; DB 4; Length 1850;
XX Best Local Similarity 60.5%; Pred No. 5,1e-112;
XX Matches 855; Conservative 0; Mismatches 547; Indels 12; Gaps 4;
XX
XX 270 CAAAACCAACGAGCAATCTACGATGCTCTGATCTCTCCGATCAAGCCGCTCTTTCT 329
XX 245 CAACAACCTCTCCCTCCGACGCGGAGCTCACTTCACAGACGTCGAAAACTCTTTT 304
XX 330 CCTTATCCCAACCTCTGATCTCCCGCTTCCACGCGGCTGTGATGCGGCGATAG 389
XX 305 CGCAGTCCCAACTACCAAACTTCTCAATCAACTGCACTCTCATGTATCCGCGTCTG 364
XX 390 GTCTTATGCTGACCTTAGGAGCGTGGTCAATGAGCTTAACTTAATGA--CGCTTGG 446
XX 365 AGCATATGTTGACCTCGGTACATGATGTTAGGTGATCTCATGAGACCAATATTC 424
XX 447 TGACGCTGAGCATGTTTAAAGGCTTGTGAAAAGTACGTTTATACCAATTTTGGCGG 506
XX 425 CTTTATGTAACATGCTATGCTTACCAACGCTGCACTTTTTCATCATTTTGTGCGG 484
XX 507 GTGAAGATCCGACGACGCGCTGAGCGGTGAGAGAGGTTTATGAGTACTGCTCTTA 566
XX 485 GAGAAGATCTATCAACCGCTGAGAAAAGTATGCGCGGTGATGAAG---CGGTTTAC 541

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QY 567 AAGGATGCTTGTCTATGGCTGCGAAGACCGCATGAGCTGTATCTTGATGATACA 626
 DB 542 GTGGATTCCTGGTTACGGCTTTGAAGATGCTCAATATACCTGCTGTATGCCAATC 601
 QY 627 TGCACAAATTCATTGCAACCAATGAAGCTGCGAATCTTTACCAACATCTCACTTACCT 686
 DB 602 TCMAAGGTTTCTTCAACCGGTGATGACAGATCGCTTCTCCATCTTGCGTAACT 661
 QY 687 CAGTGTGTGAAGATATGCGCATTTGCAATTAAGTCTTCTGAAAGAGAGAGAGATC 746
 DB 662 TTGTGATTTGAAATTAATCTGCAATATGTCATTAAGTCTTGAAGAAATGATGATTT 721
 QY 747 TCGTGGTGGGAATACAAAGTCCGAACTCAAACTCATGAAAGCTCAATGCTTTC 806
 DB 722 TCGTGAATGAGCAAGAAAGACCTTCAATTTGTTTACATGAAGCAAGATCATTTGC 781
 QY 807 CGGTTTTCGCCAATGAGTCTCTTACCAACAACTCAAAACCGGAAACCGTTAACCG 866
 DB 782 CAATTTCTCTGAGTCAAGTCTTTGACATACAAAGAGACCAAGCCATTACAG 841
 QY 867 CGGAAGAGAAAGGAGCTCGAAGAGCTCATGAAAGATTCAGAAATCTGTAGAAAT 926
 DB 842 CAGAAAGAGAGATGATCTTGAATCTTGAACAAGAGATTCCTTGAAGCTTGTCAAGAAAT 901
 QY 927 GCCAAGATCCAAATGACATTTGATTTGATGCGGAAGACAAATCCTCCAAACCGGGA 986
 DB 902 GTGTGAGAGCAATATTCATATTTGATTTGATGCTGAAATCACTTCACTTCACTGCTCA 961
 QY 987 TCGATTAACATGCTTTTATCATGCGGATCATGTTCAATGCTCAAAAGCCGAAACG 1046
 DB 962 TTGATTAATCTTACTTACTCTTCTGCTATTTATGATACAAAGGTGAAGAAC--CCTATG 1018
 QY 1047 TTACAAACAGATTCAGGCGTACTTGAAGAGACCGCGTGAAGAGACTGATTTGGCAGTAC 1106
 DB 1019 TGTGGAACCTTCAGACTTATTTGAAGATGCTAAGAGAGAAATGTTGTTGGCATCA 1078
 QY 1107 AAAATGCTGAAGAAAGATTTCTCTATGCGGTTCAAGTTGTTGAGAGGCGTTTACATCT 1166
 DB 1079 AGGCTGCTGAAGAAATGGGATACCAATGGGATTAAGTTGTTGAAGGTGCTTATATGT 1138
 QY 1167 CTAGCGAAGCTAGCTTGGCGATTTCCCTGGTGTGAAGTGGCAGTCCGACACAAATTC 1226
 DB 1139 CTAGTGAAGAAATTTGGCTGATTTGGGTTATCTCTTCCAAATCAATTAACATATTA 1198
 QY 1227 AGGATTAATCTTGTATCAATGATTTGATGACATTTCTGATGAGAAAGATCAACG 1286
 DB 1199 AGGATACACATAGTGTTCATGATTTCAATTAATGATGCTTGAAGATTTGCTAATG 1258
 QY 1287 GTTCTGGTTTGGTGTCTCTGCAACACATACGCTGATTCGGGAGAACTTGGGTGCA 1346
 DB 1259 GTCTGTGT--GAGTTGTCTTGTGCACTCAATCAATGATCAAGAAATTTGGCTGTG 1315
 QY 1347 GGAAGAGAGTGAACCTGGGATCGATTAACAGAGCGGAAGATGAGTTGCAAGCTAT 1406
 DB 1316 CAAAGACATGATTAAGGATTTGAAGAGGTGAACCATTAAGATGAAATTTGACAACTAT 1375
 QY 1407 ATGTATGATGATGATTTGCTTCTGGGTTAAGAGAGGCTTCAATGTTAGCAAGT 1466
 DB 1376 ATGGAATGCTGAGGCTATCTTTTGTGTTAAGCAATGAGGCTTTCAAGTTAGCAAT 1435
 QY 1467 ACATGCCGTTTGAACCGCTGCAACCGCTATACCGTATCTTCCGACCGCTTATGAGA 1526
 DB 1436 ATATGCCATTTGGCTGTGAGACCTGTTATGCAATACCTTTGAGAAAGGCTGAGAGAGA 1495
 QY 1527 ACCGGGAATGATGAGCCCGAGCTCAGACCTGATCATGAGAGATGAGAACTTAAGA 1586
 DB 1496 ATAGAGAGTGTGGCTGATCAGGCTTTGACAGGCAACTGATGAGAAAGAGTGTGTCA 1555
 QY 1587 GGAATTAATCGCCGGGATTTGCTTAAAGAGAGATGAGGCAATTAATGAATTTGGA 1646
 DB 1556 GGAAGATTAAGTCTTGTGCTTTAAATTTGTTGAGTGAAGTTGATGAGATTAATTAATGT 1615
 QY 1647 AATGTAGATGAATTAATTTCTTATGTAAGTTTA 1680

DB 1616 AGGCAAGGCTTCAACCATTTCTGTACAAATTA 1649
 RESULT 10
 ABL93291/C
 ID ABL93291 standard; cDNA; 475 BP.
 XX
 AC ABL93291;
 XX
 DT 10-JUN-2002 (first entry)
 XX
 DE Arabidopsis thaliana nucleic acid sequence Ref:2027056 SEQ ID NO:56.
 XX
 KW Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;
 XX genetic modification; gene; ss.
 OS Arabidopsis thaliana.
 XX
 PN US2002023280-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 26-JAN-2001; 2001US-00770444.
 XX
 PR 27-JAN-2000; 2000US-0178502P.
 XX
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAM/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T K.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GAR/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HORB/) HORBAN P.
 XX
 PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX
 DR WPI; 2002-267486/31.
 XX
 PT New Arabidopsis thaliana nucleic acid, for identifying homologous genes,
 PT producing compositions that modulate the expression or function of its
 PT encoded protein, and mapping functional regions of a protein.
 PT
 PS Claim 1; SEQ ID NO 56; 44pp; English.
 XX
 CC The present invention describes an Arabidopsis thaliana nucleic acid (1)
 CC comprising a sequence capable of hybridising under stringent conditions
 CC to a sequence (s1) selected from any one of the 999 sequences given in
 CC ABL93291 to ABL94234. (1) have insecticide and fungicide activities, and
 CC they can be used as protein expression modulators. (1) can be used in
 CC identifying homologous or related genes, in producing compositions that
 CC modulate the expression or function of their encoded proteins, mapping
 CC functional regions of the proteins, and in studying associated
 CC physiological pathways. (1) can also be used: (1) for the genetic
 CC manipulation of cells, particularly plant cells; (2) in screening assays
 CC of various plant strains to determine the strains that are best capable
 CC of withstanding a particular disease or environmental stress; (3) for
 CC enhancing or inhibiting production of a biosynthetic product in a plant;

(4) as probes in mapping and in diagnosis, in genetic modification and for screening purposes, to generate additional copies of the nucleic acids, to generate ribozymes or antisense oligonucleotides, and as single-stranded DNA probes or as triple-strand forming oligonucleotides; and (5) for generating genetically modified transgenic organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site

Sequence 475 BP; 125 A; 94 C; 140 G; 116 T; 0 U; 0 Other;

Query Match 23.9%; Score 438.4; DB 6; Length 475;

Best Local Similarity 96.6%; Pred. No. 7.4e-103;

Matches 460; Conservative 0; Mismatches 11; Indels 5; Gaps 1;

10 AAAAAAAAAAGGATTAACCGAAACATCAAGCAAAACAAAAAGAGAAATTA 69
 473 AAAAAAAAAAGGATTAACCGAAACATCAAGCAAAACAAAAAGAGAG- - - - -AATTT 419
 Db TTTTCTTTTGTGTTTGTGTTTCAAAACAAATCTTTGAATTTATGCAACCCGCTTCT 129
 Qy TTTTCTTTTGTGTTTGTGTTTCAAAACAAATCTTTGAATTTATGCAACCCGCTTCT 129
 Db TTTTCTTTTGTGTTTGTGTTTCAAAACAAATCTTTGAATTTATGCAACCCGCTTCT 359
 Qy 130 CCGAACAACCTTATCCGCGCATCTTACCGTTTACCCGCTTTAGCCGCGTGGCTCTCC 189
 Db 358 CCGAACAACCTTATCCGCGCATCTTACCGTTTACCCGCTTTAGCCGCGTGGCTCTCC 299
 Qy 190 CACGCTGCTGCTTCCACCGCGCTGCTGCGGAGATTCTGCTTGTGCAACAGAGACC 249
 Db 298 CACGCTGCTGCTTCCACCGCGCTGCTGCGGAGATTCTGCTTGTGCAACAGAGACC 239
 Qy 250 GGAACCACTTCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 309
 Db 238 GGAACCACTTCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 179
 Qy 310 CGATCAACGCGCTTCTTCTCTATCCCAACCTCTGATCTCTCTGCTTCCACCGCTT 369
 Db 178 CGATCAACGCGCTTCTTCTCTATCCCAACCTCTGATCTCTCTGCTTCCACCGCTT 119
 Qy 370 GTTGATGCTGCGCGGAGATGCTTCTATGCTGAGCTTGAAGGAGCGTGGCTGAGCTTAA 429
 Db 118 GTTGATGCTGCGCGGAGATGCTTCTATGCTGAGCTTGAAGGAGCGTGGCTGAGCTTAA 59
 Qy 430 ACTTATGAGCGCTTCTGCTGAGCGCTGGATGCTTTTGGGCTTGTGAAAAGTACGT 485
 Db 58 ACTTATGAGCGCTTCTGCTGAGCGCTGGATGCTTTTGGGCTTGTGAAAAGTACGT 3

RESULT 11

AA87063 standard; DNA; 2596 BP.

AA87063;

09-OCT-2001 (first entry)

M. sativa Pdh gene.

Pdh gene; proline dehydrogenase; alfalfa; transgenic plant; drought; proline level; environmental stress; high salinity; temperature; ds.

Medicago sativa.

WO200153323-A2.

26-JUN-2001.

10-JAN-2001; 2001WO-IL000026.

24-JAN-2000; 2000US-00490454.

(UTRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

(AGRI-) AGRIC RES ORG VOLCANI CENT.

XX Stein H, Zilberstein A, Miller G, Kapulnik Y;
 PI MPI; 2001-48333/52.
 XX Novel isolated nucleic acid used to create transgenic plants with
 PT increased proline levels and resistance to environmental stress e.g. high
 PT salinity, drought.
 XX Claim 3; Page 97-98; 99pp; English.
 PS This sequence encodes the Medicago sativa (alfalfa) proline dehydrogenase
 CC (PDH) of the invention. The PDH gene is used to create transgenic plants
 CC with increased proline levels and which is therefore resistant to
 CC environmental stress. Environmental stress conditions are high salinity,
 CC extreme temperature or drought

Sequence 2596 BP; 768 A; 443 C; 537 G; 848 T; 0 U; 0 Other;

Query Match 15.3%; Score 279.6; DB 4; Length 2596;

Best Local Similarity 59.2%; Pred. No. 1.5e-61;

Matches 594; Conservative 0; Mismatches 314; Indels 96; Gaps 3;

681 TTAGCTCAGTGTGTTGAGATTAAGTCACTTGTCTCAATTAAGTCTTGAACGATGA 740
 Db 1259 TAAGCTTGTGATTTGTGAAGTATTAAGTCAATATGTCATGATGTTGCTGAAGATGA 1318
 Qy 741 GGGATCTGCTGCGGGGGAATTAAGTCAATCTTCAATCTTCAATCTTCAATCTTCAAT 800
 Db 1319 GTGATTTGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1378
 Qy 801 CGTTTCCGCTTCTCCGATGAGTCTCTCTACCAACCAACTCAGAACCGGACCGT 860
 Db 1379 CATTCGCAATTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1438
 Qy 861 TAAACCGGGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 920
 Db 1439 TAAACCGGGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1498
 Qy 921 GGAATGCAAGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 980
 Db 1499 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1558
 Qy 981 CCGCATGATTAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1040
 Db 1559 CTGCTATGATTAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1615
 Qy 1041 CAATGCTTAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1100
 Db 1616 CTATGCTTAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1675
 Qy 1101 CAGTCAAAATGCTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1160
 Db 1676 CATCAAAAGGCTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1735
 Qy 1161 AATGCTAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1220
 Db 1736 ATATGCTAGGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1795
 Qy 1221 CAATTCAGGATCACTCTGTTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1280
 Db 1796 CTATTAAGATACATATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGAT 1855
 Qy 1281 CAACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1329
 Db 1856 CTAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1912
 Qy 1330 -----GGGAGACTTGGCTGAGAGAAAGAGTAACTCTGGAGTC 1370
 Db 1913 AATATGAT 1972
 Qy 1330 -----GGGAGACTTGGCTGAGAGAAAGAGTAACTCTGGAGTC 1370

Db 1973 TAATTAATGATTTTGTATAGAAATTTGGCTGCTGCAAAAACACATGATTAAGGATG 2012
Qy 1371 ATAAACAGACCGGAGATAGATTGTTGCAACGCTATATGTTATGTCAGATCATTGCTT 1430
Db 2033 GAAAGATGACCATTAAGATGAAATTTGCAACAATATGATGATGCTGAGCAGCTATCTT 2092
Qy 1431 TCGGGTTAAAGAGACAGGGTTCAATGTTAGCAATACATGCGGTTGGACCGGTCGAA 1490
Db 2093 TTGGTTTAAAGCAATGAGGTTTCAAGTTTACAGATATATGCTATTTGCTCTTGAGAG 2152
Qy 1491 CCGCTATACCGTATCTTCTCCAGCGCTTATGAGAACCGGAGATGATGCGCACCGAG 1550
Db 2153 CTGTTATGCAATACCTCTTGAAGAGGCTGAGAGATAGAGAGATGTTGCTGATCAG 2212
Qy 1551 CTCATGACCGTCACTCATGAGATGAGAACTTAAGAGAGATTA 1594
Db 2213 GCTTGAACGCACTGATGAGATTAATAATTTCAAAAAATTTA 2256

RESULT 12

ADA70473
ID ADA70473 strand: DNA; 1227 BP.

ADA70473;

20-NOV-2003 (first entry)

Rice gene, SEQ ID 3796.

Plant; bacterial infection; fungal infection; viral infection; rice;
gene; db.

Oryza sativa.

MO200300898-A1.

03-JAN-2003.

22-JUN-2001; 2001MO-IB001105.

22-JUN-2001; 2001MO-IB001105.

(SYGN) SYNGENTA PARTICIPATIONS AG.

Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
Katagiri F, Quan S, Tao Y, Whiteham S, Xie Z, Zhu T, Zou G;

WPI; 2003-175290/17.

Identifying at least one gene involved in plant resistance or response to
pathogenic infection for conferring resistance or tolerance to a plant to
bacterial, fungal or viral infection by determining or detecting plant
gene expression.

Claim 6; SEQ ID NO 3796; 899bp; English.

The present invention relates to a method (M1) for identifying genes
involved in plant resistance or response to pathogenic infection. M1
comprises identifying a gene whose expression is significantly altered in
the incompatible interaction of plant gene expression relative to
expression of the gene in an uninfected plant, in a mutant plant that
does not express a gene associated with response to pathogenic infection,
or in a corresponding incompatible or compatible interaction. (M1) is
useful for conferring resistance to resistance or tolerance to a plant to
bacterial, fungal or viral infection. The present sequence was used to
illustrate the invention.

Sequence 1227 BP; 196 A; 405 C; 426 G; 198 T; 0 U; 2 Other;

Query Match 14.1%; Score 258; DB 7; Length 1227;

Best Local Similarity 55.3%; Pred. No. 4, 1e-56;
Matches 563; Conservative 2; Mismatches 457; Indels 12; Gaps 4;

Qy 563 GGGATGCTTGTCTATGAGCTCGAACAACGCCATGAGCGCTGATCTTGTGATGATACATG 628
Db 7 GGGATCTGAGCTACCGGATCGAGAGCGCGAGAGCGCGCTGCGAACCGCC 66
Qy 629 CAACATTCATTCGAACCATTAAGCTGCAATCTTTTACAACTCATCTTAAGTCA 688
Db 67 GCGGATCTCTGCGCGCATGAGCGTCCGCGCGGCTGC---CTCTGGCTCGGAGGC 123
Qy 689 GTGCTTGAAGATTAATCTCCATTGTCCATTAGCTTTCTGAACAGAGTGCATCTG 748
Db 124 GTGTGATCAAGATCAAGCGGCTGTGCGCTGCGCTGCGCTGGAAGAGCGATGATCG 183
Qy 749 CTGCGTGGAAATACAAAGTCCGAATCTCAACTCTCAATGAAAGTCAATCTGTTCCG 808
Db 184 CTGCGTGGCAAG 243
Qy 809 GTTTTCTCGAATCGAGTCTTCTTCAACAACAACCTCAAGACCGGAACGTTAACCGCG 868
Db 244 GTGCTGTGCTCTCCAGCCGCTGTAACCTGAGCGCGCGAGCGCGCTGAGAGCG 303
Qy 869 GAAAGAAAGAGAGCTCGAAGAGCTCAAGAGGATTCAGAAATCTGTAGAAATGC 928
Db 304 GAG 363
Qy 929 CAAGATCCATGATCAATGTTGTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 988
Db 364 CCGAGATGAGATCCGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 423
Qy 989 GATTATAGCTTATTCATGCGAGATCAATGTTCAATGCTGCAAGAGAGAGAGAGAG 1048
Db 424 GACTACTTCAAGTTCGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 480
Qy 1049 TACAAACAGATTCAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1108
Db 481 CAGGAG 540
Qy 1109 AATGCTGAG 1168
Db 541 GCGGCGAG 600
Qy 1169 AGGAG 1228
Db 601 CCGGAG 660
Qy 1229 GATATCTACTCTTGTATCAATGATGATGATGATGATGATGATGATGATGATGAT 1288
Db 661 GACACCCAG 720
Qy 1289 TCTGTTGAG 1348
Db 721 GCGG---CGGCGAG 777
Qy 1349 AAG 1405
Db 778 AGGAG 837
Qy 1406 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1465
Db 838 ATGAG 897
Qy 1466 TACATGCTTGTGAG 1525
Db 898 TACCTGCGTGAAG 957
Qy 1526 AACCGGAG 1585
Db 958 AACAGGAG 1017
Qy 1586 AGGAGATTAATGAG 1619
Db 1018 AGGAGATTAATGAG 1051

RESULT 13
AB216299
ID AB216299 standard; DNA; 2000 BP.
XX
AC AB216299;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4104.
XX
OS Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
KM Arabidopsis thaliana.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026665.
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCEI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Krepe J, Wang X, Zhu T;
XX
DR WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 4104; 577bp + Sequence listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising: (a) contacting nucleic acid
representative of expressed polynucleotides in the plant cell with an
array or probes representative of the plant cell genome; and (b)
detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the
production of transgenic plants, cells and seeds and in producing plants
with increased tolerance to abiotic stress. The present sequence is that
of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
in methods of the invention. Note: The sequence data for this patent is
not represented in the printed specification but is based on sequence
information supplied to Derwent by the European Patent Office
XX
SQ Sequence 2000 BP; 753 A; 339 C; 244 G; 664 T; 0 U; 0 Other;
Query Match 8.2%; Score 151; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.1e-28;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCGTTTGAAGAAAAACGCGATTAACCGGAACATCAAGCAACAAAAAAGAGAA 60
DB 1850 AGCGTTTGAAGAAAAACGCGATTAACCGGAACATCAAGCAACAAAAAAGAGAA 1909
QY 61 GAGAAATATATTTTTTTTGGTTTGGTTTCAAAAAACAAATCTTGAATTTTAGGCAAC 120
DB 1910 GAGAAATATATTTTTTTTGGTTTGGTTTCAAAAAACAAATCTTGAATTTTAGGCAAC 1969
QY 121 CCGTCTTCTCCGAAACAACCTTATCCGGCGA 151
DB 1970 CCGTCTTCTCCGAAACAACCTTATCCGGCGA 2000

RESULT 14
ADA69271
ID ADA69271 standard; DNA; 2000 BP.
XX
AC ADA69271;
XX
DT 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 2594.
XX
KM Plant; bacterial infection; fungal infection; viral infection; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
pathogenic infection for conferring resistance or tolerance to a plant to
bacterial, fungal or viral infection by determining or detecting plant
gene expression.
XX
PS Claim 27; SEQ ID NO 2594; 899bp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
involved in plant resistance or response to pathogenic infection. M1
comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
illustrate the invention.
XX
SQ Sequence 2000 BP; 753 A; 339 C; 244 G; 664 T; 0 U; 0 Other;
Query Match 8.2%; Score 151; DB 7; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.1e-28;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCGTTTGAAGAAAAACGCGATTAACCGGAACATCAAGCAACAAAAAAGAGAA 60
DB 1850 AGCGTTTGAAGAAAAACGCGATTAACCGGAACATCAAGCAACAAAAAAGAGAA 1909
QY 61 GAGAAATATATTTTTTTTGGTTTGGTTTCAAAAAACAAATCTTGAATTTTAGGCAAC 120
DB 1910 GAGAAATATATTTTTTTTGGTTTGGTTTCAAAAAACAAATCTTGAATTTTAGGCAAC 1969
QY 121 CCGTCTTCTCCGAAACAACCTTATCCGGCGA 151
DB 1970 CCGTCTTCTCCGAAACAACCTTATCCGGCGA 2000

RESULT 15
ABN84373
ID ABN84373 standard; cDNA; 1494 BP.
XX
AC ABN84373;
XX
DT 01-OCT-2002 (first entry)
XX
DE Mouse proline dehydrogenase coding sequence.
XX
KM Proline dehydrogenase; PRODH; enzyme; mouse; schizophrenia;
obsessive compulsive disorder; bipolar disorder;

QY 1211 GTCCACGACAAATTACAGANTACTGCTTTGTAAGATGATGTGATCAATTCCTGATG 1270

Db 1078 ATCAACCTTACATATGAGCCACCAATCTATATGACAGAGTGCCTTAATATGTTCTG 1137

QY 1271 GAGAAAGCATCAAAAGGTTCTGTTTCGGTGTCTTCGCAACATATACGCTGATTCG 1330

Db 1138 GAGGAGCTGAAGCAGACAGCACCAGGCAAGATGATGTGGCTTCCACACAGAGGACAC 1197

QY 1331 GGGAGACTTGGGTGAGGAAAGGAGTACCTCGGGATCGATTAACAGACGGGAAGTA 1390

Db 1198 GTGCACCTTCACTTGTGACAGATGAAGAGATAGGCTGTGCATCTCGTATGTGTCAAGTGTG 1257

QY 1391 GAGTTTGACAGCTATATGATGTATGTACAGATGATGTGCTTCCTCGGGTTAAAGAGCAGAG 1450

Db 1258 TGCTTCGGACAGCTCTGTGGGATGTGTATCCAAATCACTTCCACTAGGCCAGGAGGC 1317

QY 1451 TTCAATGTTAGCAATACATGCGCTTTGGAACCCGTGCAACCGCTATACCGTATCTTCTC 1510

Db 1318 TTTCTCTGTGTAAGATATGTGCTCATGTGGCCCTGTATGAGAGTACTCCCTTAACCTGTCC 1377

QY 1511 CGAGCGCTTATGAGAACCGGGGAATGATGCGCACCGAGCTCATGACCGTCAACTATG 1570

Db 1378 CGCCCTGCTCTGGAGAACAGCAGCATCATGAAGGCTGTCAAGCAGAGAGGCAAGCTGCTTA 1437

QY 1571 AGGATGCAACTTAAGAGAGATTAATGCCCCGGA 1604

Db 1438 TGGCAGAGACTTCCGAGGCGGGCTGCGCACTGGCA 1471

RESULT 2

```

1 Sequence 7 Application US/09277262
2 Patent No. 6395482
3 GENERAL INFORMATION:
4 APPLICANT: Karayiorgou, Maria
5 APPLICANT: Gogos, Joseph A
6 TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
7 OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
8 TO INVENTION: THERETO
9 FILE REFERENCE: 600-1-2223 CIP
10 CURRENT APPLICATION NUMBER: US/09/277,262
11 CURRENT FILING DATE: 1999-03-26
12 EARLIER APPLICATION NUMBER: 09/229,530
13 EARLIER FILING DATE: 1999-01-13
14 NUMBER OF SEQ ID NOS: 9
15 SOFTWARE: PatentIn Ver. 2.0
16 SEQ ID NO 7
17 LENGTH: 2240
18 TYPE: DNA
19 ORGANISM: Mus musculus
20 US-09-277-262-7

```

Query Match	6.7%;	Score 123.6;	DB 4;	Length 2240;
Best Local Similarity	48.7%;	Pred. No. 2.3e-25;		
Matches 367;	Conservative	1;	Mismatches 380;	Indels 6;
				Gaps 1;

Qy	851	CCGAAACCGTTAAACCGCGGAAAGAAAGGAGGCTCGAAGACACTATGGAAGATTCA	910
Dy	1020	CTCTCAAGGTTCACTGAGGAGGAAGACAGACAGATGAAGAAAGATGCTCGAGAGATTGAT	1078
Qy	911	GAATCTGTAGAGAAATGCCAAGAGTCACATGTACCTATTGTGATTGATGCGGAAGACA	970
Dy	1080	GTACTGAGCCAAAGAAAGCAAAAGAAACAGATGTGGCGCTGATTGATTGTGTGACGAGGC	1139
Qy	971	ATCTCTCAAACCGCGATGATTAACATGAGCTTATTCAATGGCGATCATGTTCAATGCTGAC	1030
Dy	1140	TACTTCCAAACAGCATCAGCGCGCTTGACCTGAGAGATGACGAGCGATTCAATGTGAT	1199
Qy	1031	AAGAGCCGACCAATGGTTTACACACGATTAGAGCGATTGTGAGAGACCGCGGTAGAGA	1099
Dy	1200	AAG-----CGGTTAATTCAACCAATTCAGAGTGTAACCTCAAGAGTGTATATGACAT	1255

QY	1091	CTGCATTGGCAGTACAAAATGCTGAGAAAAGAGATGTTCTTATGGGGTTCAAAATTGGT	1150
Db	1254	GTCACCTTGGATATGGAACCTGGCTCCGCCGTGAGGGCTGTGTGTTCCGGGGCCAGCTGGTA	1313
QY	1151	AGAGGGGCTTACATGTCTACGGAAGTGAAGCTTGGCGGATTCCTGGGTTGCAAGTCGCCA	1210
Db	1314	CGTGTGCATACATGAGGGCCCAAGAGCCGTGTACAGGGCACAAGATCGGTTATGAAAGACCC	1373
QY	1211	GTCCACGACCAATTTCAAGATACTCACTCTTGTATCAATGATTTGATGACATTCCTGATG	1270
Db	1374	ATCAACCTTACTATGAAAGCCACCAATGTCTATGTACACAGGTGCTTAACTATGTTCTG	1433
QY	1271	GAGAAAGCATCAAAAGGTTCTGTTTGGGTGTGTTTCCGACACATTAACGCTGATTCG	1330
Db	1434	GAGAGGCTGAAGCACACACACCAAGCAGAAAGTATGGTGTGTTCCCAACAGAGACACC	1493
QY	1331	GGGAGACTGGCGTGGAGGAAAGCCAGAGACCTCGGAGTCGATTAACAGAAAGGGAAGTA	1390
Db	1494	GTGCATCTTCAKTTGTGTGCAAGATGAAAGATAGGCTGTGATCCTGCTGATGTGTCAAGTG	1553
QY	1391	GAGTTTGCACAGCTATATATGTTATGTCAATGATGTCATGTTCTTCGGGTTTAAAGAGACAGG	1450
Db	1554	TGCTTCCGACAGCTGCTGGGGATGTGTGACCAATCAGCTTCCACCATAGGCGACAGGCG	1613
QY	1451	TTCAATGTTAGCAAGTACATGCGCGTTTGGACCGGTCGCAACCGGTATACCGTATCTTCTC	1510
Db	1614	TTTCTCTGTGACAGATATGTGTCCCTTATGGCCCTGTATGTATAGTAACTTCCCTTAAGCTGTCC	1673
QY	1511	CGACGCGCTTATAGAAACCGGGGAATATGGCCACCGGAGCTCTAAGACGTTGAACCTCATG	1570
Db	1674	CGCGGTGCTCCGTGAGAAACAGCAGCATCATGAAGGGTCTCTAGCGAGAGAGGCAAGCTCTA	1733
QY	1571	AGGATGGAAGCTTAAAGAGAGATTATGTGCGCGGGA	1604
Db	1734	TGGCAGAGGCTCCGCAAGCGCGCTCCGCACTTGGCA	1767

RESULT 3

```

: Sequence 1 Application US/092717262
: Patent No. 6395482
: GENERAL INFORMATION:
: APPLICANT: Karayiorou, Maria
: TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
: OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
: TITLE OF INVENTION: THEREETO
: FILE REFERENCE: 600-1-1223 CIP
: CURRENT APPLICATION NUMBER: US/09/277,262
: CURRENT FILING DATE: 1999-03-26
: EARLIER APPLICATION NUMBER: 09/229,530
: EARLIER FILING DATE: 1999-01-13
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1551
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-277-262-1

```

Query Match	5.8%	Score 107.2;	DB 4;	Length 1551;
Best Local Similarity	47.7%;	Pred. No. 1e-20;		
Matches 350;	Conservative 0;	Mismatches 378;	Indels 6;	Gaps 1;

Query Match	5.8%	Score 107.2	DB 4	Length 1551
Best Local Similarity	47.7%	Pred. No. 1e-20		
Matches 350	Conservative 0	Mismatches 378	Indels 6	Gaps 1

QY	857	CCGTTAACCGCGAGAGAGAAAGGAGACTCGAAGACCTCATGAGAGATTCAAAATC	916
Db	787	CGGTTCACTGAGAGAGAGAGAGCTCAATATACCGAGATGTATACGGATGATGCTCG	846
QY	917	TGTAGAAATGCAAGAGCTCAATGTACCATTTGTTATGTATGCGGAGACAAATCCTC	976
Db	847	GCCAGAAAGCACAGAGATGGGGGTGCGGCTGATGTGATATCCGACAGACCTAATTC	906
QY	977	CAACCCGCAGTCGATTACATGCGCTTATTCATCGCGCATCATGTTCAATCTTGACAAAGAC	1038

DB 907 CAGCCGCGCATCAGCCGCTGAGCGCTGAGATGACGGAATTCATATGGAGAA---- 962
QY 1037 CGACCAATCTGTTTACAAACAGATTCAGCGCTACTTGAAGACCGCGGTGAGACTGCAT 1096
DB 963 --GCCGCTCATCTTCAACATACATACAGTGTACTCAAGATGCTGTATGACATGTGACC 1020
QY 1097 TTGGCACTACAAATGCTGAGAAAAGAAATGTTCTTATGGGTTTCAAGTTGTGAGAGG 1156
DB 1021 CTGAGCTGAGGCTGCTGCGCGTGAAGGGCTGTGTTTGGGGCAAGCTGTGGGGGC 1080
QY 1157 GCTTACATGCTTACGAGACGTAGCTTGGCGGATTCCTTGGGTTTCAAGTGCAGTCCAC 1216
DB 1081 GCATACCTGCGCCAGAGCGAGCGCCCGTGGCGAAGATCGGCTATGAGACCCCATCAAC 1140
QY 1217 GACCAATTCAGATCTACTCTTTTTCATATGATTTGATGACATTCCTGATGAGAAA 1276
DB 1141 CCCACGTACGAGGCCACCAACGCCATGTACCAAGTGGCTTGAAGTCTAGTTTGAAGAG 1200
QY 1277 GCATCAACGCGTTGCTGCTTGGTGTGCTGCTGCAACATACATACGCTATTCGGGGAGA 1336
DB 1201 CTGAGACCAACGCCAGGCCAAGTATGATGTGCTTCCCAATGAGACACAGTGC 1260
QY 1337 CTGCGTCGAGAAAACGAGTGAACCTCGGATTCGATTAACAGACGGGAATAGACTTT 1396
DB 1261 TTGCGACTGCGAGATGAGAGAGCTGGGCTGCATCCTGCTGACACACAGTGTACTTT 1320
QY 1397 GCAACGCTATATGCTATGCTGATGATGCTTCTTGGGTTTAAAGAGAGAGGTTCAAT 1456
DB 1321 GACACGCTGCTAGGAGTGTGACCAATGATGATCTTCCGCTGGGCGACGGCGCTACCCC 1380
QY 1457 GTTAGCAATGATATGCTTGTGAACCCGTCGCAACCGCTATACCGTATCTTCTCCAGCG 1516
DB 1381 GTTACAGATGATGCTTATGCTTATGCTGCTGCTGATGAGAGTGTGCTTGTGCTGCT 1440
QY 1517 GCTTATGAGAACCGGGGATATGAGCCACCGAGCTATGACCTCACTCATGAGATG 1576
DB 1441 GCCCTGAGAAACAGAGCCTCATGAGGCAACCATGCGAGCGAGTGTGCTGCTG 1500
QY 1577 GAACCTTAGAGAG 1590
DB 1501 GAGCTCTTAGAGCG 1514

RESULT 4

US-09-277-262-9
; Sequence 9, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karayiorou, Maria
; APPLICANT: Gogos, Joseph A
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 2389
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-277-262-9

Query Match 5 8%; Score 107.2; DB 4; Length 2389;
Best Local Similarity 47.7%; Pred 1.3e-20;
Matches 350; Conservative 0; Mismatches 378; Indels 6; Gaps 1;
QY 857 CCGTACCGCGAGAGAAAGGAGCTCGAAGCGCTCATGAGAGATTCAAGAAATC 916

DB 1233 CCGTCACTGAGAGAGAGAGCTACAGATGACAGATGCTACAGCGGATGATGCTCTG 1292
QY 917 TGTAGAAATGCGAAGATCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 976
DB 1293 GCCAAGAAAGCCACAGATAGGCGCTGCGGCTGATGATGATGATGATGATGATGATGAT 1352
QY 977 CAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1036
DB 1353 CAGCGGCGATGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1408
QY 1037 CGACCAATCTGTTTACAAACAGATTCAGCGCTACTTGAAGACCGCGGTGAGACTGCAT 1096
DB 1409 --GCCGCTCATCTTCAACATACATACAGTGTACTCAAGATGCTTATGAGACATGTGACC 1466
QY 1097 TTGGCACTACAAATGCTGAGAAAAGAAATGTTCTTATGGGTTTCAAGTTGTGAGAGG 1156
DB 1467 CTGAGCTGAGCTGCTGCGCGTGAAGGGCTGTGTTTGGGGCCAACTGTGGGGGC 1526
QY 1157 GCTTACATGCTTACGAGACGTAGCTTGGCGGATTCCTTGGGTTTGAAGTCCCACTCCAC 1216
DB 1527 GCATACCTGCGCCAGAGAGAGCGCGTGGCGAGATCGGCTATGAGAGACCCCATCAAC 1586
QY 1217 GACCAATTCAGATCTACTCTTTTTCATATGATTTGATGACATTCCTGATGAGAAA 1276
DB 1587 CCCACGTACGAGGCCACCAACGCCATGTACCAAGTGCCTGAGCTACGTTGTGAGAGAG 1646
QY 1277 GCATCAACGCGTTGCTGCTTGGTGTGCTGCTTCCGCAACATACATACGCTATTCGGGAGA 1336
DB 1647 CTGAGACCAACGCCAGGCCAAGTATGATGTGCTTCCCAATGAGAGACAGTGGCG 1706
QY 1337 CTGCGTCGAGAAAACGAGTGAACCTCGGATTCGATTAACAGACGGGAATAGACTTT 1396
DB 1707 TTGCGACTGCGAGATGAGAGAGCTGGGCTGCATCCTGCTGACACACAGTGTACTTT 1766
QY 1397 GCAACGCTATATGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1456
DB 1767 GACACGCTCTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1826
QY 1457 GTTAGCAATGATATGCTTGTGAACCCGTCGCAACCGCTATACCGTATCTTCTCCAGCG 1516
DB 1827 GTTACCAATGATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1886
QY 1517 GCTTATGAGAACCGGGGATATGAGCCACCGAGCTATGACCTCATGAGAGATG 1576
DB 1887 GCCCTGAGAAACAGAGCCTCATGAGGCAACCATGCGAGCGGCAAGTGTGCTG 1946
QY 1577 GAACCTTAGAGAG 1590
DB 1947 GAGCTCTTAGAGCG 1960

RESULT 5

US-09-023-655-378
; Sequence 378, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA: US/09/023,655

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWIT

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 378:

SEQUENCE CHARACTERISTICS:

LENGTH: 917 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: SINTBST01

CLONE: 1501023

US-09-023-655-378

Query Match 4.8%; Score 87.2; DB 4; Length 917;

Best Local Similarity 47.9%; Pred. No. 4,4e-15;

Matches 251; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

1067 TACTTGAAGAGAGCCGCTGAGAGACTGCTATTGGCAAGTACAAATAGCTGAGAAAGAGAT 1126

5 TACCTCAAGAGATGCCATATGATGACCCCGATGTGAGACTGCTGCGCTAGGAGC 64

1127 GTTCTATGGGGTTCAAGTTGGTGAAGAGGGCTTACATGTCTAGCGAAAGCTTGGCG 1186

65 TGGTGTGTTGGGGCCAGCTGTGGCGGGCGCATACCTGGCCAGAGCGAGCCCGTGGC 124

1187 GATTCCCTGGGTTGCAAGTGGCAAGTCCAGACACACATTCAGAGTACTCACTCTTTTAC 1246

125 GCAGAGATGGCTATAG 184

1247 AATGATGTATGACATCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1306

185 CACAGAGTGGCTGAGTACGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244

1307 CTGCGAACAATACGCTGATTCGGGAGAGACTTGGCTGAGAGAGAGAGAGAGAGAGAG 1366

245 GTGGCTCCCAATAG 304

1367 ATGATTAACAG 1426

305 CTGATCTGCTGAGACAG 364

1427 TCTTGGGTTAAG 1486

365 AGTCTCCGCTGGGAG 424

1487 GCAACGCTATACCGTATCTTCCGAGCGGCTTATGAGAGAGAGAGAGAGAGAGAGAGAG 1546

425 ATGAGAGTGTGCTGCTATCTTGTCCGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 484

1547 GAGCTCATACCGTCACTCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590

485 ACCCATCGGAG 528

APPLICANT: DORNER, F.

APPLICANT: SCHEITLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLEPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313

FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300

TELEFAX: (703) 683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: pTZgpt-F1s

US-08-232-463-14

Query Match 3.2%; Score 58.6; DB 1; Length 7218;

Best Local Similarity 1.3%; Pred. No. 2.7e-06;

Matches 4; Conservative 198; Mismatches 107; Indels 0; Gaps 0;

67 TTAATTTTGTGTTTGGTTTCAAAAACAAATCTGATTTATGCAACCGCTC 126

1132 YYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYY 1191

127 TCTCCGACAACTTATTCGGGAGCTTACCGTTACCGCTTAAACCGGAGTCC 186

1192 YYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYY 1251

187 TCCACCGTACAGCTTCCACCGCGCGTCCGAGATTCCTCTGAGACAAAGC 246

1252 YYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYY 1311

247 ACCGGAACACTCTTACACCAACCAACCGAGCAATCTACAGAGTCTCATCT 306

1312 YYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYY 1371

307 CTCGATCAAGCCGCTTTTCTCTCTATCCCACTCTGATCTCTCTGATCAACGC 366

1372 YYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYTYY 1431

367 GATGTTGCA 375

1432 YYYGTACCA 1440

RESULT 6

US-08-232-463-14

Sequence 14; Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:

QY 1513 ACGGCTTATGAGAACCGGGAGATGATGCCACCGGAGCTCATGACCTGATCATGAG 1572
Db 5795 CAGATTGAAAGAACGCGGTTGCTCGGCACCTTCACAAAAGAAATTAACCTTGCA 5854
QY 1573 GATGAACTTAAGAGAGATTAATGCGCGGAT 1605
Db 5855 GAAGAGTTGCTGGCGCTCTCGTAGAGAGGAT 5887

RESULT 9
US-09-645-055-56
; Sequence 56, Application US/09645055
; Patent No. 6599701
; GENERAL INFORMATION:
; APPLICANT: CLARITY BIOSCIENCES, INC.
; APPLICANT: Honeycutt, Rhonda
; APPLICANT: McClelland, Michael
; TITLE OF INVENTION: IDENTIFYING ORGANISMS BY DETECTING
; FILE REFERENCE: 475402000100
; CURRENT APPLICATION NUMBER: US/09/645,055
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/150,977
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-09-645-055-56

Query Match 2.5%; Score 45.6; DB 4; Length 1393;
Best Local Similarity 56.8%; Pred. No. 0.0058;
Matches 84; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1578 AACTTAAGAGAGATTAATCGCCGGATGCTTAAGAGAGATGAGCCATTAATG 1637
Db 667 ATCTTGTACTTATTTATGAGAAATGCTCAAAACATAGTGTGATATATGTAATG 726
QY 1638 AATTGGGAATGTGATGATTAATTTCTTATGATGATTAAGAAATGAAAAA 1697
Db 727 AATTGGAATGAGAGATTAATAAATTTGAAAAATATATTTCCATTTTATCTATA 786
QY 1698 AATTATATATTAAGAAATGAGTAGTA 1725
Db 787 CATTAATTAATAAATACTACTAGTA 814

RESULT 10
US-09-645-055-55
; Sequence 55, Application US/09645055
; Patent No. 6599701
; GENERAL INFORMATION:
; APPLICANT: CLARITY BIOSCIENCES, INC.
; APPLICANT: Honeycutt, Rhonda
; APPLICANT: McClelland, Michael
; TITLE OF INVENTION: IDENTIFYING ORGANISMS BY DETECTING
; FILE REFERENCE: 475402000100
; CURRENT APPLICATION NUMBER: US/09/645,055
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/150,977
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-09-645-055-55

Query Match 2.5%; Score 45.6; DB 4; Length 1481;
Best Local Similarity 56.8%; Pred. No. 0.0061;
Matches 84; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1578 AACTTAAGAGAGATTAATCGCCGGATGCTTAAGAGAGAGATGAGCCATTAATG 1637
Db 697 ATCTTGTACTTATTTATGAGAAATGCTCAAAACATAGTGTGATATATGTAATG 756
QY 1638 AATTGGGAATGTGATGATTAATTTCTTATGATGATTAAGAAATGAAAAA 1697
Db 757 AATTGGAATGAGAGATTAATAAATTTGAAAAATATATTTCCATTTTATCTATA 816
QY 1698 AATTATATATTAAGAAATGAGTAGTA 1725
Db 817 CATTAATTAATAAATACTACTAGTA 844

RESULT 11
US-10-204-708-40/c
; Sequence 40, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: BERLIN, Kurt
; APPLICANT: BIRKENBERG, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 40
; LENGTH: 19513
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-40

Query Match 2.5%; Score 45.6; DB 4; Length 19513;
Best Local Similarity 60.5%; Pred. No. 0.028;
Matches 75; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 22 ATAAACCGAATCATACCAACAAAAAGAGAGAAATTAATTTTGT 81
Db 3020 ATTAACTTACATATACCTTATCTATACACCAAAAAATATATCTTTTTTTTT 2961
QY 82 TTGCTTCAAAACAAATCTTGAATTTATGCAACCGCTCTCCGAAACACTT 141
Db 2960 TTTTCTTTTAAACAAATATATACATCTTATCCATCAATCTTAACCTCTAAC 2901
QY 142 TATC 145
Db 2900 AAAC 2897

RESULT 12
US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 593827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
US-08-487-826B-13

STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
FILING DATE:
CLASSIFICATION:
Prior Application Data:
APPLICATION NUMBER: 08/901,127
FILING DATE:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
Prior Application Data:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION:
Prior Application Data:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP35.1.FWCCL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
FAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-09-299-268-51

Query Match 2.3%; Score 41.6; DB 3; Length 810;
Best Local Similarity 49.1%; Pred. No. 0.061;
Matches 110; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Db 1610 TAAAGAGAGTATGAGCCATTAAATGAAATTGGAAATGTAGATGAATTAATTTCTTC 1669
387 TATATTGGGATTCCTGATACCTATATCATATTCGTATATGCTATATAGAAATTTTTC 446
Qy 1670 TATGTAGTTTAAAGAAATTGAAACAAAATTTATATATAGAAATGAGTAGTAAAGAA 1729
447 TACAGTGTATGATTAAGAAATAGACGAAGATATTAATCTATATAAATTTGATTAATGAT 506
Db 1730 CATTTCCGTGGCTAAATATTTTCATGAGGACTATGTTTTTACTATCAATATATCAT 1789
507 TGTGTATGTTCTCTATATATTTGATTTCCGCTTATATGTTTATATGATGAGAGAT 566
Qy 1790 CACAAATGATATATTCACCTTATCAATATAAATGCTTTTACTTT 1833
Db 567 TGTAGCTTATATACATCTATATATTTAGACATCTGTGCTCT 610

RESULT 15
US-08-307-499-1/c
Sequence 1, Application US/08307499
Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a

TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:
CLASSIFICATION: 435
Prior Application Data:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
Prior Application Data:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
Prior Application Data:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP35.1.FWCCL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
FAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14176 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 3852..4226
FEATURE:
NAME/KEY: CDS
LOCATION: 4585..4887
FEATURE:
NAME/KEY: CDS
LOCATION: 5131..5310
FEATURE:
NAME/KEY: CDS
LOCATION: 5760..5912
FEATURE:
NAME/KEY: CDS
LOCATION: 6786..7130
FEATURE:
NAME/KEY: CDS
LOCATION: 10148..10513
US-08-307-499-1

Query Match 2.3%; Score 41.6; DB 1; Length 14176;
Best Local Similarity 49.1%; Pred. No. 0.33;
Matches 110; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Qy 1610 TAAAGAGAGTATGAGCCATTAAATGAAATTGGAAATGTAGATGAATTAATTTCTTC 1669
Db 1820 TATATTGGGATTCCTGATACCTATATCATATTCGTATATGCTATATAGAAATTTTTC 1761
Qy 1670 TATGTAGTTTAAAGAAATTGAAACAAAATTTATATATAGAAATGAGTAGTAAAGAA 1729

Db 1760 TACAGTGTAGATTAGAAATAGACGAAGTATAAATCTATATAAATGTATTATGAT 1701
 QY 1730 CATTTCCTGTGGCTAAATATTTTTCATGAGGAGCTAAGTTTACTATCATATATATCAT 1789
 Db 1700 TGTGTATGTCTCTAATATATGTGATCCGCTCTATATGTTCTAATATGATAGCGAGAT 1641
 QY 1790 CACAATGTATATTCACCTTATCATATAAATAGCTTTTACTTT 1833
 Db 1640 TGTAGCTTAAATACATCTAATATATTAGACATCTGTGCTCT 1597

Search completed: March 10, 2004, 12:07:08
 Job time : 133.386 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2004, 10:27:40 ; Search time 598.434 Seconds
(Without alignments)
11202.658 Million cell updates/sec

Title: US-10-026-767-3

Perfect score: 1833
Sequence: 1 agcgttagaagaaaaaacgc.....ataaaatgcttttctt 1833

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1833	100.0	1833	14 US-10-026-767-3	Sequence 3, Appl1
2	1457.8	79.5	1461	9 US-09-938-842A-1411	Sequence 111, Ap
3	1457.8	79.5	1461	11 US-09-938-842A-1411	Sequence 141, Ap
4	1280.6	69.9	1339	9 US-09-770-445-11	Sequence 56, Appl
5	438.4	23.9	475	9 US-09-770-444-56	Sequence 11, Appl
6	315.2	17.2	1001	12 US-10-424-599-116395	Sequence 116395,
7	294.8	16.1	2000	12 US-10-424-599-91151	Sequence 91151, A
8	158.6	8.7	806	12 US-10-424-599-30413	Sequence 30413, A
9	151	8.2	2000	9 US-09-938-842A-4104	Sequence 4104, Ap
10	151	8.2	2000	11 US-09-938-842A-4104	Sequence 4104, Ap
11	125.8	6.9	609	12 US-10-424-599-27121	Sequence 27121, A
12	123.6	6.7	1494	13 US-10-119-635-3	Sequence 3, Appl1
13	123.6	6.7	2240	13 US-10-119-635-7	Sequence 7, Appl1
14	119.4	6.5	121	15 US-10-307-005-989	Sequence 989, App
15	119.4	6.5	121	15 US-10-307-005-990	Sequence 990, App

16	119.4	6.5	121	15	US-10-307-005-997	Sequence 997, App
17	119.4	6.5	121	15	US-10-307-005-998	Sequence 998, App
18	119.4	6.5	121	15	US-10-307-005-1001	Sequence 1001, Ap
19	119.4	6.5	121	15	US-10-307-005-1002	Sequence 1002, Ap
20	119.4	6.5	121	15	US-10-307-005-1005	Sequence 1005, Ap
21	119.4	6.5	121	15	US-10-307-005-1006	Sequence 1006, Ap
22	117.8	6.4	121	15	US-10-307-005-993	Sequence 993, App
23	117.8	6.4	121	15	US-10-307-005-994	Sequence 994, App
24	117.8	6.4	780	12	US-10-424-599-30414	Sequence 30414, A
25	111.4	6.1	992	12	US-10-424-599-115698	Sequence 115698,
26	107.2	5.8	1551	13	US-10-119-635-1	Sequence 1, Appl1
27	107.2	5.8	2389	13	US-10-119-635-9	Sequence 9, Appl1
28	105.8	5.8	2565	15	US-10-104-047-285	Sequence 285, App
29	89.2	4.9	435	12	US-10-424-599-62358	Sequence 62358, A
30	80.8	4.4	335	12	US-10-425-114-10387	Sequence 10387, A
31	68	3.7	567	9	US-09-917-800A-1203	Sequence 1203, Ap
32	58.8	3.2	465	10	US-09-918-995-4291	Sequence 2291, Ap
33	57.4	3.1	413	9	US-09-960-352-14086	Sequence 14086, A
34	53.4	2.9	433	9	US-09-917-800A-231	Sequence 231, Appl
35	49.8	2.7	3673778	14	US-10-312-841-1	Sequence 1, Appl
36	48.8	2.7	1438	15	US-10-369-493-75906	Sequence 25906, A
37	46.8	2.6	5539	14	US-10-240-485-179	Sequence 179, App
38	46.4	2.5	7589	14	US-10-240-453-263	Sequence 263, App
39	45.6	2.5	19513	12	US-10-221-613-206	Sequence 206, App
40	45.6	2.5	19513	14	US-10-204-708-40	Sequence 40, Appl
41	45.2	2.5	5250	14	US-10-311-455-2175	Sequence 2175, Ap
42	45.2	2.5	139257	10	US-09-920-671-11	Sequence 11, Appl
43	45	2.5	6112	14	US-10-311-455-636	Sequence 636, App
44	45	2.5	14649	14	US-10-239-676-121	Sequence 121, App
45	45	2.5	14649	14	US-10-240-453-141	Sequence 141, App

ALIGNMENTS

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RESULT 1
US-10-026-767-3
Sequence 3, Application US/10026767
Publication No. US20030014774A1
GENERAL INFORMATION:
APPLICANT: Hitachi, LTD.
APPLICANT: Riken
APPLICANT: Japan International Research Center for Agricultural Science
APPLICANT: Bio-oriented Technology Research Advancement Institute (BRAIN)
TITLE OF INVENTION: Transgenic rice plant and its family with environmental
TITLE OF INVENTION: stress resistant by proline accumulation of high level and its
FILE OF INVENTION: production.
FILE REFERENCE: NT01P0353
CURRENT APPLICATION NUMBER: US/10/026,767
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 3
LENGTH: 1833
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: 113...1612
AUTHORS: Tomohiro Kiyasu, Yoshu Yoshida, Kazuko Yamaguchi-
AUTHORS: Shinozaki, Kazuo Shinozaki
TITLE: Title : A nuclear gene encoding mitochondrial proline
TITLE: dehydrogenase, an enzyme involved in proline metabolism, is
TITLE: upregulated by proline but downregulated by dehydration in
TITLE: Arabidopsis.
JOURNAL: The Plant Cell
PAGES: 1323-1335
DATE: 1996-05-27
DATABASE ACCESSION NUMBER: D83025
DATABASE ENTRY DATE: 1995-12-25
US-10-026-767-3
Query Match 100.0%, Score 1833, DB 14, Length 1833,
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTTAAAGAAAAACAGCGATMAAACCGAATCTCAAGCAAAACAAAAAAGAGAA 60
Db 1 AGGCTTAAAGAAAAACAGCGATMAAACCGAATCTCAAGCAAAACAAAAAAGAGAA 60
QY 61 GAGAAATATTTTTTTTTTCTGTTTCAAAAACAAATCTTGAATTTTATGCAAC 120
Db 61 GAGAAATATTTTTTTTTTCTGTTTCAAAAACAAATCTTGAATTTTATGCAAC 120
QY 121 CGCTCTTCCGAAACAATTTATCCGCGATTTACCGTTTACCGCTTTAGCCGAT 180
Db 121 CGCTCTTCCGAAACAATTTATCCGCGATTTACCGTTTACCGCTTTAGCCGAT 180
QY 181 GGGGCTCCCAACCGTGTCTTCCACCGCGCTGCTCCGAGATTTCTCTCTTGAACA 240
Db 181 GGGGCTCCCAACCGTGTCTTCCACCGCGCTGCTCCGAGATTTCTCTCTTGAACA 240
QY 241 ACAAGCAACGGAACCACTCTTCAACCAACCAACCAACCAACCAACCAACCAAC 300
Db 241 ACAAGCAACGGAACCACTCTTCAACCAACCAACCAACCAACCAACCAACCAAC 300
QY 301 CGATCTCCGATCAAGCCGCTTTCTCTCTATCCCAACCTGTATCTCTCCGTTCC 360
Db 301 CGATCTCCGATCAAGCCGCTTTCTCTCTATCCCAACCTGTATCTCTCCGTTCC 360
QY 361 CACCGCGCTGTGATGCGGCGGATAGGTCTTATGCTGATGGAAGCACTGGATCAT 420
Db 361 CACCGCGCTGTGATGCGGCGGATAGGTCTTATGCTGATGGAAGCACTGGATCAT 420
QY 421 GAGCTCTAACTTATGACGCTTCCGAGCGGATGAGCGTGTGAGGCTGTGAAG 480
Db 421 GAGCTCTAACTTATGACGCTTCCGAGCGGATGAGCGTGTGAGGCTGTGAAG 480
QY 481 TAGCTTTATGACCAATTTTGCAGCGGTGAAGATGCGACGACCGCTGAGCGCTGAG 540
Db 481 TAGCTTTATGACCAATTTTGCAGCGGTGAAGATGCGACGACCGCTGAGCGCTGAG 540
QY 541 AAGGCTTTATGAGACTTCTGTCTTAAAGGATGCTGTCTATAGGCGTGAAGACGCGA 600
Db 541 AAGGCTTTATGAGACTTCTGTCTTAAAGGATGCTGTCTATAGGCGTGAAGACGCGA 600
QY 601 TGAGCGCTGTATCTGTATGATTAATGATGAACATTCATTCGAACATTTAGCTCCAA 660
Db 601 TGAGCGCTGTATCTGTATGATTAATGATGAACATTCATTCGAACATTTAGCTCCAA 660
QY 661 ATCTTTACCAACATCTCACTTATGCTGATGCTGTGTAAGATTAATCTTGTGCAAT 720
Db 661 ATCTTTACCAACATCTCACTTATGCTGATGCTGTGTAAGATTAATCTTGTGCAAT 720
QY 721 TAGCTCTGTAAGAGAGAGAGATGCTGCGGTGGAATACAAAGTCCGACTTCA 780
Db 721 TAGCTCTGTAAGAGAGAGAGATGCTGCGGTGGAATACAAAGTCCGACTTCA 780
QY 781 ACTCTCATGAGAGCTCAATCTGTTCCGCTTTCTCCGAATCGATCTCTTACCAAC 840
Db 781 ACTCTCATGAGAGCTCAATCTGTTCCGCTTTCTCCGAATCGATCTCTTACCAAC 840
QY 841 AAACCTCAAGACCGGAAACGTTTACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 AAACCTCAAGACCGGAAACGTTTACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 AAGATTCAGAAATCTGTAGAGAAATGCGAAGATCCATGTACATTTGATGATGTC 960
Db 901 AAGATTCAGAAATCTGTAGAGAAATGCGAAGATCCATGTACATTTGATGATGTC 960
QY 961 GGAAGACAAATCTCCCAACCGGATGATTAATGCTATTCATGCGGATCATGTT 1020
Db 961 GGAAGACAAATCTCCCAACCGGATGATTAATGCTATTCATGCGGATCATGTT 1020
QY 1021 CAATCTGACAAAGACGCAATGCTTTACCAACGATTCAGGCGTATGAGAGCGC 1080
Db 1021 CAATCTGACAAAGACGCAATGCTTTACCAACGATTCAGGCGTATGAGAGCGC 1080

Db 1021 CAATCTGACAAAGACGCAATGCTTTACCAACGATTCAGGCGTATGAGAGCGC 1080
QY 1081 CGGTGAGAGAGCTCATTTGGCACTTACCAAAATGCTGAGAAAGAGATGTTCTATGCGGTT 1140
Db 1081 CGGTGAGAGAGCTCATTTGGCACTTACCAAAATGCTGAGAAAGAGATGTTCTATGCGGTT 1140
QY 1141 CAATGCTGAGAGAGGCTTACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 CAATGCTGAGAGAGGCTTACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 CAATGCTGAGAGAGGCTTACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1201 CAATGCTGAGAGAGGCTTACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 ATTCTGATGAG 1320
Db 1261 ATTCTGATGAG 1320
QY 1321 CGCTGATTCGGGAG 1380
Db 1321 CGCTGATTCGGGAG 1380
QY 1381 CGGAGAGATGAG 1440
Db 1381 CGGAGAGATGAG 1440
QY 1441 GAG 1500
Db 1441 GAG 1500
QY 1501 GTATCTTCTCCGAGCGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 GTATCTTCTCCGAGCGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TCACTCATGAG 1620
Db 1561 TCACTCATGAG 1620
QY 1621 TATGAGAGCTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1621 TATGAGAGCTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 AGAATTCAG 1740
Db 1681 AGAATTCAG 1740
QY 1741 GCTAAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 GCTAAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 ATTCACTTATCAATTAATGCTTTTACTTT 1833
Db 1801 ATTCACTTATCAATTAATGCTTTTACTTT 1833

RESULT 2

US-09-938-842A-1411
Sequence 1411, Application US/09938842A

Patent No. US20020160378A1
GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A

PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16


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QY 351 TCCTCCGTTCCACCGCGGCTGCTGATGCGCGCGGATGCTCTATGATGCGA 410
Db 1 TCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
QY 411 CGGCGGCTGATGAGCTCTAACTTATGAGCGCTTCGCGTGAAGCGTGGCAAGT 470
Db 61 CGTGGGCTGATGAGCTCTAACTTATGAGCGCTTCGCGTGAAGCGTGGCAAGT 120
QY 471 TTGTGAAAAGTACGTTTATGACCAATTTTTCGCGCGCGTGAAGTGCAGAGCG 530
Db 121 TTGTGAAAAGTACGTTTATGACCAATTTTTCGCGCGCGTGAAGTGCAGAGCG 180
QY 531 AGGCGGCTGAGAGCGTTTATGAGCTACGCTTAAAGGATGCTTCTATGCGCTG 590
Db 181 AGGCGGCTGAGAGCGTTTATGAGCTACGCTTAAAGGATGCTTCTATGCGCTG 240
QY 591 AACACGCGGATGAGCGCTTATCTTGATGATGATGATGATGATGATGATGATG 650
Db 241 AACACGCGGATGAGCGCTTATCTTGATGATGATGATGATGATGATGATGATG 300
QY 651 AAGCTGCGCAATCTTTACCAACATCTCACTTTAGCTCACTGCTGCTGCTGCT 710
Db 301 AAGCTGCGCAATCTTTACCAACATCTCACTTTAGCTCACTGCTGCTGCTGCTG 360
QY 711 TTGTGCAATTAAGCTTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 770
Db 361 TTGTGCAATTAAGCTTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 771 CGAATTCGAATCTCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 830
Db 421 CGAATTCGAATCTCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 831 TCTACCAACAACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
Db 481 TCTACCAACAACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 891 CAGCTCATGAGAGAGATTCAGAAATCTGTAGAGAGAGAGAGAGAGAGAGAG 950
Db 541 CAGCTCATGAGAGAGATTCAGAAATCTGTAGAGAGAGAGAGAGAGAGAGAG 600
QY 951 TGAATGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1010
Db 601 TGAATGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 1011 CGATCATGTTCAATGCTGACCAAGACCGACCAATCTTACCAACAGATTGAG 1070
Db 661 CGATCATGTTCAATGCTGACCAAGACCGACCAATCTTACCAACAGATTGAG 720
QY 1071 TGAAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
Db 721 TGAAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 1131 CTATGAGGAGTCAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1190
Db 781 CTATGAGGAGTCAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 1191 CCTGAGGAGTCAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
Db 841 CCTGAGGAGTCAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 1251 ATTGTATGAGATTCCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1310
Db 901 ATTGTATGAGATTCCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 1311 CAACACATTAACGCTGATTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1370
Db 961 CAACACATTAACGCTGATTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1371 ATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1430
Db 1021 ATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
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QY 1431 TCAGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1490
Db 1081 NCGNNNTNNNAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1491 CGCGTATACGCTATCTCTCCGAGCGCTTATGAGAGAGAGAGAGAGAGAGAG 1550
Db 1141 CGCGTATACGCTATCTCTCCGAGCGCTTATGAGAGAGAGAGAGAGAGAGAG 1200
QY 1551 CTCAATGACCGTCAACCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1610
Db 1201 CTCAATGACCGTCAACCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1611 AAAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1670
Db 1261 AAAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1671 ATGTAGTTTAAAGAAATTGA 1689
Db 1321 ATGTAGTTTAAAGAAATTGA 1339
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RESULT 5

US-09-770-444-56/c

Sequence 56, Application US/09770444

Patent No. US20020023280A1

GENERAL INFORMATION:

APPLICANT: Gorlach, Jörn

APPLICANT: An, Yong-Qiang

APPLICANT: Hamilton, Carol M.

APPLICANT: Price, Jennifer L.

APPLICANT: Raines, Tracy M.

APPLICANT: Yu, Yang

APPLICANT: Ramezani, Joshua G.

APPLICANT: Mathew, Abraham V.

APPLICANT: Ledford, Brooke L.

APPLICANT: Woessner, Jeffrey P.

APPLICANT: Haas, William David

APPLICANT: Garcia, Carlos A.

APPLICANT: Krieger, Maja

APPLICANT: Slader, Ted

APPLICANT: Davis, Keith R.

APPLICANT: Allen, Keith

APPLICANT: Hoffman, Neil

APPLICANT: Hurban, Patrick

TITLE OF INVENTION: Expressed Sequences of Arabidopsis

FILE REFERENCE: 2027 (Para-016PRV)

CURRENT APPLICATION NUMBER: US/09/770,444

CURRENT FILING DATE: 2001-01-28

PRIOR APPLICATION NUMBER: 60/178,502

PRIOR FILING DATE: 2000-01-27

NUMBER OF SEQ ID NOS: 999

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 56

LENGTH: 475

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-770-444-56

Query Match 23.9%; Score 438.4; DB 9; Length 475;

Best Local Similarity 96.6%; Pred. No. 1.8e-103;

Matches 460; Conservative 0; Mismatches 11; Indels 5; Gaps 1;

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QY 10 AAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 69
Db 473 AAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
QY 70 TTTTCTTTGTTTCTGTTTCAAAAACAAATCTTGAATTTTATGAGCAACCGCTCT 129
Db 418 TTTTCTTTGTTTCTGTTTCAAAAACAAATCTTGAATTTTATGAGCAACCGCTCT 359
QY 130 CGAACAACCTTTATCCGCGAGATCTTACCGTTTACCGCGGTTAGCCGCGTCTCT 189
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Db 358 CGAAGCAATTTATCGGCGATCTCACCGTTTACCGCTTTAGCCCGATGGATCTCC 299
 QY 190 CACCGTGA CTGCTTCCACCGCGCTGTCCGGAATCTCTCTTGTGACAACAAGACC 249
 Db 298 CACCGTGA CTGCTTCCACCGCGCTGTCCGGAATCTCTCTTGTGACAACAAGACC 239
 QY 250 GGAACCACTCTTCCACCGCGCTGTCCGGAATCTCTCTTGTGACAACAAGACC 309
 Db 238 GGAACCACTCTTCCACCGCGCTGTCCGGAATCTCTCTTGTGACAACAAGACC 179
 QY 310 CGATCAAGCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 369
 Db 178 CGATCAAGCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 119
 QY 370 GTTGCATGCGCGCGGCGATGAGTCTTGTGATGAGTCTTGTGATGAGTCTTGTG 429
 Db 118 GTTGCATGCGCGCGGCGATGAGTCTTGTGATGAGTCTTGTGATGAGTCTTGTG 59
 QY 430 ACTTATGACGCTTGTGATGAGTCTTGTGATGAGTCTTGTGATGAGTCTTGTG 485
 Db 58 ACTTATGACGCTTGTGATGAGTCTTGTGATGAGTCTTGTGATGAGTCTTGTG 3

RESULT 6

US-10-424-599-116395
 ; Sequence 116395, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223) B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 116395
 ; LENGTH: 1001
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_76115C.1
 US-10-424-599-116395

Query Match

Best Local Similarity 62.6%; Pred. No. 3,1e-71;
 Matches 526; Conservative 0; Mismatches 308; Indels 6; Gaps 2;

QY 762 ACAAAAGTCGAACTCTCATGAGAGCTCAAAATCGTTCCGGTTTCTCCGAT 821
 Db 2 ACAAGAGACCTTGTTCAGTTGATGAGAGCAAGATGCTTCCCATATCTCCGAT 61
 QY 822 CGAGTCTCTTCAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 881
 Db 62 CAAGCCCTTGTACCAACAACAACAACAACAACAACAACAACAACAACAACAACA 121
 QY 882 AGCTCGAAGAGTCAATGAGAGATTCAGAAATCTGAGAAATGCCAAGATCCATG 941
 Db 122 ACTTCAACTTGCATCCAGAGATTCAGAAATCTGAGAAATGCCAAGATCCATG 181
 QY 942 TACATTTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
 Db 182 TTTCTTTGTGATGAG 241
 QY 1002 ATTCATGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1061
 Db 242 ACTCTCTGCAATCTTGACA---CAAGATGACAACCCCAATGATGATGATGATGAT 298
 QY 1062 AGCGTACTTGAG 1121

Db 299 AGACTACTCTCAAGAGATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 358
 QY 1122 AGAATTTCTTATGAGGCTTCAAGTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1181
 Db 359 TGGGAATCCCAATGAGGCTTCAAGTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 418
 QY 1182 TGGCGAATCCCTGAGGCTTCAAGTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1241
 Db 419 TGGCTGAGCTTTTGGGCTATTTCTTCCCAATTCAGAGAGAGAGAGAGAGAG 478
 QY 1242 GTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1301
 Db 479 GTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 535
 QY 1302 TCGTTTGGCAACATTAAGCTGATGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1361
 Db 536 TTTTCTTCAACTCATTAATGTTGAGTCAAGGAGAGAGAGAGAGAGAGAGAGAG 595
 QY 1362 TCGGATCGATAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1421
 Db 596 TAGGATGAGAAAG 655
 QY 1422 CATTTCTTCTCGGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1481
 Db 656 CACTTCTTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 715
 QY 1482 CCGTCCCAACCGCTATACCGTATCTTCTCGAGCGGCTTATGAGAACCGGAGATGATG 1541
 Db 716 CAGTGAAGCTGTATAGCATATCTTAAAGAGGCTTAAGAGAGATGAGAGATGATG 775
 QY 1542 CCACCGAGCTATGACCGCTCACTCACTGAGAGATGAGAGATGAGAGATGAGAG 1601
 Db 776 CTGCTTCCGCGCTTGTACAGGCACTGATGAGAGAGAGAGAGAGAGAGAGAGAG 835

RESULT 7

US-10-424-599-91151
 ; Sequence 91151, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223) B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 91151
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_5331C.1
 US-10-424-599-91151

Query Match

Best Local Similarity 50.8%; Pred. No. 9.4e-66;
 Matches 834; Conservative 0; Mismatches 797; Indels 11; Gaps 5;

QY 92 AAAACAATCTTGAATTTATGCAACCGCTTCTCCGAACAACCTTTATCCGCGA 151
 Db 150 AAAACAATCTTGAATTTATGCAACCGCTTCTCCGAACAACCTTTATCCGCGA 209
 QY 152 TCTTACCGTTTACCGCTTCTTACCGCTTCTTACCGCTTCTTACCGCTTCTTAC 211
 Db 210 CTCCTTCAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 269
 QY 212 GTCGTCGAGAGATGCTCTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271
 Db 270 ATGCCCCACCGTCACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329

QY 272 AAACCCACGAGCAATCTCAGATGCTCTGATCTCCGATCAAGCCGCTTTTCC 331
 DB 330 AACTTCAGACTATGAGAGACGCGCAATTTCACTTCAGACGCGGAGCGCTTTCCG 389
 QY 332 TCTATCCCAACCTTGATCTCTCCGTTCCACCGCGGTGTGATGCGGCGCATAGT 391
 DB 390 TCAGATGACGAGAAAGCTGCTCCGGCTCTCCGCTTTTGCATGCGACGCGGTGGG 449
 QY 392 CCTATGTCGACTAGGAGCGTGGTCTATGACTCTTAACTTATGACGCTTGATACG 451
 DB 450 CCAATGTAACCTGGAGATGTGTGATGAAAGTCTCCGGTTCAGACCGGCTCCG 509
 QY 452 CGTGGCACTGTTTAAAGGCTTGTGAAAAGTACTTTATGACATTTTGGCGGTGAA 511
 DB 510 AAGGATCTCATATGCGCCGACAGAGAGAGAGTCTTCTGCGACTTCTGGCGGAG 559
 QY 512 GATGCGACGACCGCGCTGAGCGGTGAGAAAGCTTTATGAGCTACTGTCTTAAAGG 571
 DB 570 GACGCGCGCGCGCGGACGAGCATCAGCGCGCTCAAGAGAG--CCGGCTTACGTGC 626
 QY 572 ATGCTGTCTATGCGGTGAGACGCGCATGACGCTGATCTGTGATGATTAACATGCA 631
 DB 627 ATGCTGTGTACGCTGTGAGAGACGCGCATGAAAACGATGGTGTGATGACCTGCA 666
 QY 632 CAATTCATTCGACCATTTGAGCTGCGAATCTTACCAATCTCACTTTAGCTCAGTG 691
 DB 687 TGCCCTATGCGCACTGTT-TAGAAAGATGATGACCTTCTTATGATGGCAAAAAA 745
 QY 692 GTTGTGAAGATTAAGCTGCTTCTCAATTAAGTCTTCTGAAAGAGAGAGAGCTGCTG 751
 DB 746 CCTTCATCTGTTTGTCTATGAAAGCAAGTCTTCTCAATTTTGGTGAAGTCTAGTC 805
 QY 752 CGGTGGATATCAAAAGTCCGAACTCTCATGAGCTCAATGCTTTCGGTT 811
 DB 806 CTTTGTACCAACAGAGAGAGACGAGCCTCTAACCCAGAGAGAGAGATGATCTTC 855
 QY 812 TTTCCGATGAGTCTCTTCTTACCAAACTCAGAACCGGAAACGTTAACCGGAA 871
 DB 866 AACTTGCACCAAGAGACTCTTGAATTTGCGCAAAATGTGAGAAAGCCAAATGCTT 925
 QY 872 GAAGAAAGGAGCTCGAAGCAGCTCATGAGAGATTC-AGAAATCTGTAGAAATGCCA 930
 DB 926 TGTGTGTGATGATTAACACACACGCGTAAACCCGCTATTTGATTAATCACTCCA 965
 QY 931 AGAGTCCATGATTCATTTGATTTGATGATGCGAAGACCAATCTCCAACCCGATCGA 990
 DB 986 CGTACCCCAAGCGCTCTGGGGGGTATGACAGAACACACAGTTCAACCGCTATGCA 1045
 QY 991 TTACATGGCTATTCATCGCGGATCATGATCTTCAATGCTGACAAAGACCGACCATCTT 1050
 DB 1046 TTACTTCACATCTCTTCTTCATTAAGCACAAATTAAGATGACAAAC--CCCATGTGTT 1102
 QY 1051 CAACACGATTCAGCGATTTGAGAGACGCGGTGAGAGACTGATTTGGCAGTACAAA 1110
 DB 1103 TGAACACATTCAGCTTATTTGAAGATGCCAGAGAGAGGTGTGTCTCAACAAAGGC 1162
 QY 1111 TGTGAGAAAGAGATGTCTATGAGGCTTCAAGTGTGTGAGAGGCTTACATGTCTAG 1170
 DB 1163 AGCGAAAAAATGGAGATTCATTTGGGTTCAATTTGATGAGGTCCCTACATGTCCAC 1222
 QY 1171 CGAAGTATGCTTGGCGATTCCTCGGGTGAATGCGCATGCGACGACGACATTCAGGA 1230
 DB 1223 AGAAGTAAATGGCTAGTATTTGGTATGATCCCAATTCACATTCATTAAGA 1282
 QY 1231 TACTCACTCTTTGATCAATGATTTGATGACATTCCTGATGAGAGAAAGCATCAACGCTTC 1290
 DB 1283 AACGACAAATTTGCTCAATGCTCTCATATTTCTTGAGAAAGTTGCTAATGATCC 1342
 QY 1291 TGTGTT---TGGGTGCTTCCGACACATTAACGCTATTCGGGGAGATTGCGCGAG 1347
 DB 1343 CGGTTCATTTCAATGTGTTCTTGTGACCTCACAATTTGAATCAGGGAAATGGCTGACG 1402

QY 1348 GAAAGCGAGTACCTCGGGATGATTAACAGAACGGGAAGTATGATTCACACTATA 1407
 DB 1403 AAAAGCATATGATTTGGGGGTGAAAGGTAAACACAAAGTATGACAACTGTA 1462
 QY 1408 TGTATGTCAGATGATGATTTGCTTCGGTTAAAGAGAGAGGTTCAATGTTAGCA 1467
 DB 1463 TGAATGTGAGAGGACCTTCTTCTTGTGATGCAATGAGGTTTCAAGTTGCAAGTA 1522
 QY 1468 CATGCCGTTTGAACCCGTCGACACCGCTATACCTGATCTTCCGACCGCTTATGAGA 1527
 DB 1523 TATGCAATTTGGCGGTATGATGATGTTATGCTTACCTTCTGAAAGGCTGAAGAAA 1582
 QY 1528 CCGGGGAATGATGAGCCACCGAGCTCATGACCGTCACTCATGAGATGAACTTAAG 1587
 DB 1583 TAGAGGCTTTTGGCTGATCAAGTTTGTATGATGCAATTTGATGAAAGAGCTTGGAG 1642
 QY 1588 GAGATTAATCGCGGATTTGCTTAAAGAGAGATGAGACCATTAATGAATTTGGAA 1647
 DB 1643 AAGATTAAGCTGCAATGTTCTTAAATTTGTCAGAAATCAGGATTCATGACTTTTGT 1702
 QY 1648 ATGTAGTAAATTAATTTCTTATGATGTTTAAAGATTTGAAATTAATTAATA 1707
 DB 1703 CAATTAAGAGCTTTGTATGTGAGAAATTTGATTCATTAATTAATTTGCTT 1762
 QY 1708 TAAGAAATGAGTATGATGAAGA 1729
 DB 1763 TGTATGTAGTGTGTTGTTGAA 1784

RESULT 8
 US-10-424-599-30413
 ; Sequence 30413, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kowalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223) B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 30413
 ; LENGTH: 806
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_127465C.1
 US-10-424-599-30413

Query Match 8.7%; Score 158.6; DB 12; Length 806;
 Best Local Similarity 57.1%; Pred. No. 1.4e-30;
 Matches 309; Conservative 0; Mismatches 229; Indels 3; Gaps 1;

QY 239 CAACAGCAACGGAAACCACTTTTCAACCAACCAAAACCCACCGAGCAATTCAGATGT 298
 DB 261 CTACTGTCTCGCTGCGCTGCTCCCGCGCTGCTCGCTCCCTCCGCGCGCTCCGACAC 320
 QY 269 CTGATCTCTCGATCAAGCCGCTTTTCTCTCTATCCCAACCTGATCTCTCCGT 358
 DB 321 CTCAGCTTCCGCGAGCTGAGAAAGCTCTTCTCTCTGCTCTCAACACAGCTCTCCGC 380
 QY 359 TCACCGCGGTGTGATGATGCGCGGCGATAGTCTTATGTGACCTTAGGAGAGCTGTC 418
 DB 381 TCTCTCGCGGTGTGACGCGCACCGCGCTCGAGCCATGTGTGACTTTCGACATGTGCTC 440
 QY 419 ATGAGCTTAACTTATGAGCTTCTGATGAGCGGTGAGCGGTGAGCTTTTAAAGGCTTGTGAA 478
 DB 441 TTGCAATTAATTCATGACAGTGTGATGACATTCGCGACCTTATCTCCACCGTCCGC 500
 QY 479 AGTACGTTTATGACCAATTTTGGCGCGGTGAGATGCGACGACGCGCTGAGCGGCTG 538

Db 501 AACACCTTTTGGACCACTTTTGGCGCGGAGGAGCGCATCACACCGCTGCCAGCATC 560
QY 539 AGAAGGTTTATGAGTACTGCTTAAAGGATGCTGTATGAGGCTGAACAGC 598
Db 561 CGCAGCT--AAACGTCGCGGCTCCGCGGCAAGCTGCTAGGGGTGAAGACCA 617
QY 599 GATGACGCTGATCTTGTGATATATACATGACCAATTCATTCGAACATGAAAGCTGCC 658
Db 618 AACGACACGACGCGCTCCAGCACTTCAAGGCTTCTTCAACATCAGCTCAGC 677
QY 659 AATCTTTACCAACATCTCACTTGAAGTGTGAGATATACATGCAATTTGTGCA 718
Db 678 AGATGCTTCCCTTCTTCTTCTGAGCTTGTGATGATGAAATACCGCATATGCTCT 737
QY 719 ATTAGCTTCTGAAACGAGTGAAGCATCTGCTGCGGTGGAAATCAAAAAGTCCGAATTC 778
Db 738 ATGAGCTGTGGAAGCAATGAGTACCTTTAGATGCAACACAGACCCCTTGTTC 797
QY 779 A 779
Db 798 A 798

RESULT 9

US-09-938-842A-4104
Sequence 4104, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krepes, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4104
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-4104

Query Match

Best Local Similarity 8.2%; Score 151; DB 9; Length 2000;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCGTTTGAAGAAACAGCGATTAACCCGAAACATCAAGCAACAAAAAAGAGAA 60
Db 1850 AGCGTTTGAAGAAACAGCGATTAACCCGAAACATCAAGCAACAAAAAAGAGAA 1909
QY 61 GAGAAATATTTTGTGTTGTTGTTTCAAAAACAATCTTGAATTTATGGAAC 120
Db 1910 GAGAAATATTTTGTGTTGTTTCAAAAACAATCTTGAATTTATGGAAC 1969
QY 121 CCGTCTTCCGAAACAACTTATCCGGCA 151
Db 1970 CCGTCTTCCGAAACAACTTATCCGGCA 2000

RESULT 10

US-09-938-842A-4104
Sequence 4104, Application US/09938842A
Patent No. US20040009476A9
GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Krepes, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4104
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-4104

Query Match

Best Local Similarity 8.2%; Score 151; DB 11; Length 2000;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCGTTTGAAGAAACAGCGATTAACCCGAAACATCAAGCAACAAAAAAGAGAA 60
Db 1850 AGCGTTTGAAGAAACAGCGATTAACCCGAAACATCAAGCAACAAAAAAGAGAA 1909
QY 61 GAGAAATATTTTGTGTTGTTTCAAAAACAATCTTGAATTTATGGAAC 120
Db 1910 GAGAAATATTTTGTGTTTCAAAAACAATCTTGAATTTATGGAAC 1969
QY 121 CCGTCTTCCGAAACAACTTATCCGGCA 151
Db 1970 CCGTCTTCCGAAACAACTTATCCGGCA 2000

RESULT 11

US-10-424-599-27121/C
Sequence 27121, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
PRIOR FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 27121
LENGTH: 609
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_124491C.1
US-10-424-599-27121

Query Match

Best Local Similarity 6.9%; Score 125.8; DB 12; Length 609;
Matches 275; Conservative 0; Mismatches 227; Indels 3; Gaps 1;
QY 1112 GCTGAGAAAGAGAAATCTTATGAGTTCAGTGTGAGAGGGGCTTACATGCTAGC 1171
Db 604 GCGAAGAAATATGAGAGTCTTAAGAGGCTTCAATATGAGTGAAGGCGCCCAATGCCCCCA 545
QY 1172 GAGCTAGCTTGGCGGATTCCTGAGTTGCAAGTGCAGATCCAGACAAATTCAGAT 1231
Db 544 AAGAGTAAATTTGGAGTCACTTGGTATGATCCCAATTTGGCAACCCCATTCAGAA 485

OY	1232	CTCACTCTGTTTCAAGATTGTATGACATCTCCATGAGGAAAGATCAACGGTCT	1291
Db	484	AAACCCATTCGTTCAAGGCGCGCCCTCATATTTTTCAGAAAMAATGAAAAAGAACCC	425
OY	1292	GGTT---TCGGTGTGTTCTCGCAACATTAACGTGATTCGGGGAGACTTGCGTGAAG	1348
Db	424	GGTTCAATTGAGTTGTTTTTCCCTCCCAATATGTTTCAAGGAAATGAGGCTTCCACC	365
OY	1349	AAAGCGATGACCTCGGGATCGATTAAAGAAACGGGAAGATGAGTTGCAACAGTATAT	1408
Db	364	AAACCCATTCATTTGGGGGTTGAAAGGTCAACCCCGCATTAATTTGCCCCCTGAT	305
OY	1409	GGTATGTGAGATGATGTCCCTTGGGGTTAAGAAGAGAGGTTCAATTTAGCAAGTAC	1468
Db	304	GGAAAGCAACAGGCCCTTTCCTTGTTGTGAACATCCAGGCTTTCTATGTGAGAAATAT	245
OY	1469	ATGCCGTTTGACCCGTCGCAACGCTATTACCGTATCTTCTCCAGCGCGCTTATGAGAAC	1528
Db	244	ATTCCTTTGGCCCCGGGAATAAGGGTATGCCCTTCCCTTCAGAAAGGGGGGAAAAAAA	185
OY	1529	CGGGAAATGATGCCACCGGAGCTCATGACCGTCACTCATGAGAGTGAACCTTAAGAGG	1588
Db	184	ACAGGGCTTTTGGTTGCTCGAGTTTATATAGCGAATTTTGAAGAAAGAGATTGGCAAGA	125
OY	1589	AGATTAAATCGCCGGATGGCGTAA	1613
Db	124	AAATTTAAAACTGCAATGTTTTTAA	100


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Db      1140 TACTTCAACACGACATGAGCCGCTGACCTCGAGATGACCGGATGATTTATGTGAT 1199
Qy      1031 AAGAGCCGACATGCTTTACACGATTCAGGCGTATCTGAGAGACCGCGTGAGAGA 1090
Db      1200 AAG-----CCGTTATCTTCAACACATTCAGTCTCAACAGAGATGCTTATGACAAAT 1253
Qy      1091 CTGATTTGGCAGTACAAATAGTCTGAGAAAGAAATGTTCTTATGAGGGTTCAAGTGGTG 1150
Db      1254 GTGACCTTGATGATGAACTGCTGCGGTGAGGGCTGTGTTCGCGGGCCAACTGTGTA 1313
Qy      1151 AAGAGGGCTTACATGCTGACGACATGCTTGGCGAATCCCTGGTTGCAAGTCCGA 1210
Db      1314 CCGTGTGATACATGAGCCCAAGAGCGGTGTGAGGGGACGACAGATCGGTTATGAAAGACCC 1373
Qy      1211 GTCCAGACACAAATCAGGATCTGACCTGTTGTAATGATGATGATGATGATGATG 1270
Db      1374 ATCAACCTTACATGAAAGCCCAAGATGCTATGTAACAGAGTGTCTTAACTATGTTCTG 1433
Qy      1271 GAGAAAGCATCAACGCTTCTGTTCTGATGCTGTTCTGCAACACATPACGCTGATTCG 1330
Db      1434 GAGAGCTGTAAGACACAGACCCAGGACAGATGATGATGATGATGATGATGATGATGATG 1493
Qy      1331 GGAAGACTTGGCTCAGAGAAAGCGATGCTCGGATTCATTAACAGAAAGGAAAGTA 1390
Db      1494 GTGCACTTCACTGTGTGAGAGATGAAAGATAGGCTGTGATGATGATGATGATGATG 1553
Qy      1391 GAGTTGACAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1450
Db      1554 TGCTTGGACAGCTCTGAGGATGTGTGACCAATACACTTCCACTAGGCGAGGACAGG 1613
Qy      1451 TTCAATGTTAGCAATGATGCTGTTGACCCGTTGCGAACCGCTTATACCTTATCTTC 1510
Db      1614 TTCTCTGTGTAACAGATGATGCTGATGCTGATGATGATGATGATGATGATGATGATG 1673
Qy      1511 CGAGCGCTTATGAGAACCGGGAGATGATGAGCACCGAGCTCAATGACCTCACTCATG 1570
Db      1674 CGCCGTGCTGAGAAACGACGATCATGAAAGGTGTCTCAGCGAGAGGACGACTGCTA 1733
Qy      1571 AGATGAACTTAAAGAGATTAATCCCGGGA 1604
Db      1734 TGGCAGAGAGCTCCGAGGCGGCTGCGCACTGGCA 1767

RESULT 14
US-10-307-005-989
; Sequence 989, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kniel
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; SOFTWARE: Friedman macro Napro4
; NUMBER OF SEQ ID NOS: 2717
; TYPE: DNA
; LENGTH: 121
; ORGANISM: Arabidopsis thaliana

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US-10-307-005-989
Query Match      6.5%; Score 119.4; DB 15; Length 121;
Best Local Similarity 99.2%; Pred. No. 7,1e-21;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      71 TTTTGTGTTTGTGTTTCAAAAACAAATCTTGAATTTATGCAACCGCTCTTC 130
Db      1 TTTTGTGTTTGTGTTTCAAAAACAAATCTTGAATTTATGCAACCGCTCTTC 60

Qy      131 CGAACAACTTTATCCGGGATCTTACCGCTTTACCGCTTTAGCCGGTGGCTCTCC 190
Db      61 TGAACAACTTTATCCGGGATCTTACCGCTTTACCGCTTTAGCCGGTGGCTCTCC 120

Qy      191 A 191
Db      121 A 121

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RESULT 15
US-10-307-005-990/c
; Sequence 990, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kniel
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 990
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-307-005-990

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Query Match      6.5%; Score 119.4; DB 15; Length 121;
Best Local Similarity 99.2%; Pred. No. 7,1e-21;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      71 TTTTGTGTTTGTGTTTCAAAAACAAATCTTGAATTTATGCAACCGCTCTTC 130
Db      121 TTTTGTGTTTGTGTTTCAAAAACAAATCTTGAATTTATGCAACCGCTCTTC 62

Qy      131 CGAACAACTTTATCCGGGATCTTACCGCTTTACCGCTTTAGCCGGTGGCTCTCC 190
Db      61 TGAACAACTTTATCCGGGATCTTACCGCTTTACCGCTTTAGCCGGTGGCTCTCC 2

Qy      191 A 191
Db      1 A 1

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Job time : 604.434 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: March 10, 2004, 10:40:15 ; Search time 4183.5 seconds
(without alignments)
13084.110 Million cell updates/sec

Title: US-10-026-767-3
Perfect score: 1833
Sequence: 1 agcgttagaagaaagcgc.....ataaagcttttacttt 1833

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: em_ectba:*
2: em_ecthum:*
3: em_ectin:*
4: em_ectmu:*
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6: em_ectpl:*
7: em_ectro:*
8: em_ect1:*
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14: gb_ect6:*
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17: em_ges_hum:*
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19: em_ges_pln:*
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23: em_ges_mus:*
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25: em_ges_rod:*
26: em_ges_phg:*
27: em_ges_vrt1:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	684.2	37.3	690	AV784199	AV784199 AV784199
2	653	35.6	664	AV823266	AV823266 AV823266
3	550.8	30.0	554	AV533853	AV533853 AV533853
4	542.2	29.6	563	AV830448	AV830448 AV830448

Result No.	Score	Query Match	Length	ID	Description
5	541.8	29.6	549	AI998362	AI998362 701545370
6	536.4	29.3	549	AV530853	AV530853 AV530853
7	517.2	28.2	746	AV959076	AV959076 LERPH17F
8	513	28.0	518	AV563245	AV563245 AV563245
9	499.4	27.2	745	CD813513	CD813513 BN15.0190
10	496	27.1	757	CD837236	CD837236 BN45.0511
11	492.4	26.9	754	CD832104	CD832104 BN40.062A
12	481.4	26.3	483	AV556853	AV556853 AV556853
13	475.4	25.9	720	CD813554	CD813554 BN15.020B
14	463	25.3	713	CD835442	CD835442 BN45.045I
15	456.4	24.9	698	CD823584	CD823584 BN25.060J
16	429.8	23.4	433	AV819304	AV819304 AV819304
17	427.4	23.3	432	AV788703	AV788703 AV788703
18	425	23.0	425	AV809949	AV809949 AV809949
19	422	22.8	520	AA568088	AA568088 28737 Lam
20	418	22.8	419	AV816969	AV816969 AV816969
21	417	22.7	420	AV805545	AV805545 AV805545
22	415.4	22.7	417	AV805031	AV805031 AV805031
23	413.2	22.5	724	CD824641	CD824641 BN25.058E
24	412	22.5	413	AV803385	AV803385 AV803385
25	411.8	22.5	740	CD825843	CD825843 BN25.061P
26	406.4	22.2	421	AV819048	AV819048 AV819048
27	403	22.0	403	AV561789	AV561789 AV561789
28	400.2	21.6	664	CD839287	CD839287 RF02.114F
29	395.6	21.6	521	AV959075	AV959075 LERPH17F
30	391.2	21.3	420	AV808518	AV808518 AV808518
31	389.4	21.2	541	AA395287	AA395287 27070 Lam
32	381.8	20.8	822	BA487028	BA487028 BOCI126TR
33	379	20.7	440	T43041	T43041 6304 Lambda
34	375.8	20.5	686	B2465331	B2465331 BONTK24TR
35	371.8	20.3	386	AV819277	AV819277 AV819277
36	371.4	20.3	381	BE524790	BE524790 M54C9STM
37	368.6	20.1	738	B2039614	B2039614 1ka29109
38	362.2	19.8	451	T41726	T41726 10307 Lambda
39	354.2	19.3	395	AV818024	AV818024 AV818024
40	353.2	19.3	370	BE521126	BE521126 M17T23XTM
41	347.8	19.0	360	BE521125	BE521125 M17T23STM
42	344.4	18.7	402	AL947958	AL947958 Arabidops
43	342	18.4	343	BE524810	BE524810 M54B8STM
44	338	18.4	342	AV533298	AV533298 AV533298
45	330.8	18.0	676	BZ007035	BZ007035 oem84e01

ALIGNMENTS

RESULT 1
AV784199/c
DEFINITION AV784199 RAF15 Arabidopsis thaliana cDNA clone RAF105-17-B01.3',
LOCUS AV784199.1 GI:19802989
ACCESSION AV784199
VERSION AV784199.1
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
AUTHORS Seki,M., Narusaka,M., Ishida,Y., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,Y., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4159
Fax: 81-298-36-9050
Email: msek@tc.riken.go.jp

TITLE
JOURNAL
COMMENT

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBlueScript vector as a Set1/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

Source

Location/Qualifiers

1..690
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL05-17-E01"
/dev_stage="rosette plants"
/lab_host="SOLR"
/clone_lib="RAFL5"
/note="Site 1: Set1; Site 2: XhoI; subjected to dehydration-treated(1,2,5,10,24 hr)"

ORIGIN

Query Match 37.3%; Score 684.2; DB 9; Length 690;
Best Local Similarity 99.6%; Pred. No. 7,3e-127;
Matches 686; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1142 AAGTGTGAGAGGAGGCTTACATGTCTAGCGAAGCTAGTGGCGATTCCCGGGTGC 1201
690 AAGTGTGAGAGGAGGCTTACATGTCTAGCGAAGCTAGTGGCGATTCCCGGGTGC 631
1202 AAGTGTGAGAGGAGGCTTACATGTCTAGCGAAGCTAGTGGCGATTCCCGGGTGC 1261
630 AAGTGTGAGAGGAGGCTTACATGTCTAGCGAAGCTAGTGGCGATTCCCGGGTGC 571
1262 TTCTGTATGAGAGAGATCAACGGTTGCTTGGGATGGTCTCGCAACAGATAC 1321
570 TTCTGTATGAGAGAGATCAACGGTTGCTTGGGATGGTCTCGCAACAGATAC 511
1322 GCTGATTCGGGAGAGTTCGCTCGAGAGAAACGAGTGCCTCGGATCGATTAACG 1381
510 GCTGATTCGGGAGAGTTCGCTCGAGAGAAACGAGTGCCTCGGATCGATTAACG 451
1382 GGGAGATAGAGTTGACAGCTATATGATATGTCAGATGCAATGTCCTTGGGTTAA 1441
450 GGGAGATAGAGTTGACAGCTATATGATATGTCAGATGCAATGTCCTTGGGTTAA 391
1442 AGAGCAGGTTCAATGTTACCAAGTACATGCCGTTTGGACCCGTCGCAACCGCTATAC 1501
390 AGAGCAGGTTCAATGTTACCAAGTACATGCCGTTTGGACCCGTCGCAACCGCTATAC 331
1502 TATCTTCCGAGCGCTTATAGAACCGGGGAATGATGCGCACCGAGCTCATGACCG 1561
330 TATCTTCCGAGCGCTTATAGAACCGGGGAATGATGCGCACCGAGCTCATGACCG 271
1562 CAACTCATGAGATGAGAACTTAAGAGAGATTAATCGCCGGGATGCGTAAAGAGAGAT 1621
270 CAACTCATGAGATGAGAACTTAAGAGAGATTAATCGCCGGGATGCGTAAAGAGAT 211
1622 ATGAGCATTAAATGAATGGAAATGAGATGAATGAATTAATTTCTTATGATTTAA 1681
210 ATGAGCATTAAATGAATGGAAATGAGATGAATGAATTAATTTCTTATGATTTAA 151
1682 GAATTTGAAAACAAAATTAATTAATTAAGAAATGAGATGAGATTAATTTCTTATG 1741
150 GAATTTGAAAACAAAATTAATTAATTAAGAAATGAGATGAGATTAATTTCTTATG 91
1742 CTAAATATTTTCTGAGGAGCTATGTTTCTATCATCATATATCATCAAAATGATA 1801
90 CTAAATATTTTCTGAGGAGCTATGTTTCTATCATCATATATCATCAAAATGATA 31
1802 TTGACCTTATCAATTAATATGCTTTTAC 1830
30 TTGACCTTATCAATTAATATGCTTTTAC 2

RESULT 2
AV823266

LOCUS AV823266 664 bp mRNA linear EST 01-APR-2002
DEFINITION AV823266 RAF5 Arabidopsis thaliana cDNA clone RAFL05-17-E01 5',
RNA sequence.
VERSION AV823266
KEYWORDS AV823266.1 GI:19865323
SOURCE EST.
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 664)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Saito, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawah, J., Itoh, M., Ishii, Y.,
Arikawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)

TITLE JOURNAL
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: meeki@rct.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBlueScript vector as a Set1/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

Source

Location/Qualifiers

1..664
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL05-17-E01"
/dev_stage="rosette plants"
/lab_host="SOLR"
/clone_lib="RAFL5"
/note="Site 1: Set1; Site 2: XhoI; subjected to dehydration-treated(1,2,5,10,24 hr)"

ORIGIN

Query Match 35.6%; Score 653; DB 9; Length 664;
Best Local Similarity 100.0%; Pred. No. 1,3e-120;
Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGCGTTGAAAAAAGACGATTAACCGAATCAATCAAGCAACAAAAAAGAGAA 60
12 AGCGTTGAAAAAAGACGATTAACCGAATCAATCAAGCAACAAAAAAGAGAA 71
61 GAGAAATATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120
72 GAGAAATATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 131
121 CGGTTCTCCGAAACAATTTATCCGCGATCTTACCGTTTACCGGCTTTAGCCGCT 180
132 CGGTTCTCCGAAACAATTTATCCGCGATCTTACCGTTTACCGGCTTTAGCCGCT 191
181 GGGTCTCCGAAACAATTTATCCGCGATCTTACCGGCTTTAGCCGCTTTAGCA 240
192 GGGTCTCCGAAACAATTTATCCGCGATCTTACCGGCTTTAGCCGCTTTAGCA 251
241 ACAAGCAGGAAACACCTCTTCAACCAACCAACCAACCAACCAACCAACCAAC 300
252 ACAAGCAGGAAACACCTCTTCAACCAACCAACCAACCAACCAACCAACCAAC 311
301 CGATCTCCGATCAAGCGGCTTTTCTCTCTATATCCCAACCTGATCTCCCGTTC 360
312 CGATCTCCGATCAAGCGGCTTTTCTCTCTATATCCCAACCTGATCTCCCGTTC 371
361 CACGCGGCTGTGATGAGCGGCGAGATGCTATGATGAGCTAGAGAGCTGGATCAT 420

Db 372 CACCGCGTGTGATGCGGCGGATGAGTCTTATGTCAGCTAAGGAGCGTGGTCTAT 431
 QY 421 GAGCTTAACCTTATGAGCGCTTGTGACGCGGATGAGCTTTTAAAGGCTTGAAAG 480
 Db 432 GAGCTTAACCTTATGAGCGCTTGTGACGCGGATGAGCTTTTAAAGGCTTGAAAG 491
 QY 481 TACGTTTATGACCAATTTTGGCGCGGTGAAGATGCGGACGCGCTGAGCGCTGAG 540
 Db 492 TACGTTTATGACCAATTTTGGCGCGGTGAAGATGCGGACGCGCTGAGCGCTGAG 551
 QY 541 AAGGTTTATGAGCACTCTGCTTAAAGGATGCTTGTATGCGGTGCAACGCCCA 600
 Db 552 AAGGTTTATGAGCACTCTGCTTAAAGGATGCTTGTATGCGGTGCAACGCCCA 611
 QY 601 TGACGCTGTATCTTGTATGATGATTAACATGCAACATTCATTGCAACATTGAG 653
 Db 612 TGACGCTGTATCTTGTATGATGATTAACATGCAACATTCATTGCAACATTGAG 664

RESULT 3
 AVS53853 554 bp mRNA linear EST 06-SEP-2000
 LOCUS AVS53853 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
 DEFINITION cDNA clone RZ74c03r 5', mRNA sequence.
 ACCESSION AVS53853
 VERSION AVS53853.1 GI:8725266
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 554)
 Aaamizu, S., Nakamura, Y., Sato, S. and Tabata, S.
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size-selected cDNA libraries
 DNA Res 7 (3), 175-180 (2000)

JOURNAL MEDLINE 20363093
 PUBMED 10907847
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 153-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
 Location/Qualifiers
 1..554
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="RZ74c03r"
 /tissue_type="roots"
 /clone_lib="Arabidopsis thaliana roots Columbia"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI"

FEATURES
 source
 ORIGIN
 Query Match 30.0%; Score 550.8; DB 9; Length 554;
 Best Local Similarity 99.6%; P-Val. 4.2e-100;
 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 935 TCCATATACCATGTTGATTTGATGAGGAGACCAATCTCCACCCGCGATTCATTC 994
 Db 1 TCCATATACCATGTTGATTTGATGAGGAGACCAATCTCCACCCGCGATTCATTC 60
 QY 995 ATGGCTTATTCATCGCGGATCGATGCTTCATGTCACCAAGACCGCAATCGTTTAAAC 1054
 Db 61 ATGGCTTATTCATCGCGGATCGATGCTTCATGTCACCAAGACCGCAATCGTTTAAAC 120
 QY 1055 ACGATTACGCGGATCGATGAGGAGCGCGGTGAGAGACTGATTTGGCAGTAAATAGCT 1114
 Db 121 ACGATTACGCGGATCGATGAGGAGCGCGGTGAGAGACTGATTTGGCAGTAAATAGCT 180

QY 1115 GAGAAAGGAATGTTCTTATGCGGTTCAAGTTGAGAGAGGGGCTTACATGTTAGCGAA 1174
 Db 181 GAGAAAGGAATGTTCTTATGCGGTTCAAGTTGAGAGAGGGGCTTACATGTTAGCGAA 240
 QY 1175 CGTACCTTGGCGGATTCCTCGGTTGCAAGTCGCGCATGCAAGACCAATTCAGATTA 1234
 Db 241 GCTACCTTGGCGGATTCCTCGGTTGCAAGTCGCGCATGCAAGACCAATTCAGATTA 300
 QY 1235 CACTCTTGTACAAATGATTTGATGACATTCCTGATGAGAAAGATGCAACGTTCTGCT 1294
 Db 301 CACTCTTGTACAAATGATTTGATGACATTCCTGATGAGAAAGATGCAACGTTCTGCT 360
 QY 1295 TTGCGTGTGTTCTTCGCAACATTAACGCTATTCGCGGAGACTTTCGTCAGGAAAGCG 1354
 Db 361 TTGCGTGTGTTCTTCGCAACATTAACGCTATTCGCGGAGACTTTCGTCAGGAAAGCG 420
 QY 1355 AGTACCTTCGGGATGATTAACAGAACCGGAGATAGATTGCAACGCTATTAAGTATG 1414
 Db 421 AGTACCTTCGGGATGATTAACAGAACCGGAGATAGATTGCAACGCTATTAAGTATG 480
 QY 1415 TCAGATGATTTGTCCTTGGGTTAAAGAGACAGAGGTTCAATGTTAGCAATGATCGCG 1474
 Db 481 TCAGATGATTTGTCCTTGGGTTAAAGAGACAGAGGTTCAATGTTAGCAATGATCGCG 540
 QY 1475 TTTGACCCGCTGCG 1488
 Db 541 TTTGACCCGCTGCG 554

RESULT 4
 AVB30448 563 bp mRNA linear EST 01-APR-2002
 LOCUS AVB30448 RAFU9 Arabidopsis thaliana cDNA clone RAFU09-69-M18 5',
 DEFINITION mRNA sequence.
 ACCESSION AVB30448
 VERSION AVB30448.1 GI:19872508
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 563)
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Setou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.
 A large scale analysis of Arabidopsis full-length cDNA (2002b)
 Unpublished (2002)

TITLE JOURNAL
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: meeki@rtc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda PUC-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified pBluescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
 details.

FEATURES
 source
 1..563
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFU09-69-M18"
 /dev_stage="plants at various developmental stages from
 germination to mature seeds"
 /lab_host="DH10B"

ORIGIN

/clone.lib="RAFL9"
/note="Site 1: BamHI; Site 2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"

Query Match 29.6%; Score 542.2; DB 9; Length 563;
Best Local Similarity 99.5%; Pred. No. 2.2e-98;
Matches 543; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 TTTAGAAAAACGAGATTAACGAAACATCAAGCAACAAAAAGAGAAGA 64
DB 17 TTGAAAAACGAGATTAACGAAACATCAAGCAACAAAAAGAGAAGA 76
QY 65 AATTAATTTTGTGTTTGTGTTTCAAAAACAAATCTTGAATTTTATGCAACCCGT 124
DB 77 AATTAATTTTGTGTTTGTGTTTCAAAAACAAATCTTGAATTTTATGCAACCCGT 136
QY 125 CTTCTCCGAAACAACTTTATCCGCGATCTTACCGTTTACCGCTTTTACCGCTTGGT 184
DB 137 CTTCTCCGAAACAACTTTATCCGCGATCTTACCGTTTACCGCTTTTACCGCTTGGT 196
QY 185 CTTCTCCGAAACAACTTTATCCGCGATCTTACCGTTTACCGCTTTTACCGCTTGGT 244
DB 197 CTTCTCCGAAACAACTTTATCCGCGATCTTACCGTTTACCGCTTTTACCGCTTGGT 256
QY 245 GCAACCGAAACCACTTTTACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 304
DB 257 GCAACCGAAACCACTTTTACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 316
QY 305 CTTCTCCGAAACCACTTTTACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 364
DB 317 CTTCTCCGAAACCACTTTTACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 376
QY 365 GCGGTGTGATCGCGCGGAGATGATGCTTATGCTTATGCTTATGCTTATGCTTATG 424
DB 377 GCGGTGTGATCGCGCGGAGATGATGCTTATGCTTATGCTTATGCTTATGCTTATG 436
QY 425 TCTAACTTATGACGCTTGTGATGACGCTTGTGATGACGCTTGTGATGACGCTTGTG 484
DB 437 TCTAACTTATGACGCTTGTGATGACGCTTGTGATGACGCTTGTGATGACGCTTGTG 496
QY 485 TTTTATGACCAATTTTGTGCGCGGATGATGCTTATGCTTATGCTTATGCTTATG 544
DB 497 TTTTATGACCAATTTTGTGCGCGGATGATGCTTATGCTTATGCTTATGCTTATG 556
QY 545 GTTTATG 551
DB 557 GTTTATG 563

RESULT 5
A1998362 549 bp mRNA linear EST 08-SEP-1999
LOCUS A1998362/6
DEFINITION 701545370 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis
thaliana cDNA clone 701545370, mRNA sequence.
ACCESSION A1998362
VERSION A1998362.1 GI:5845267
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosales; Euphorbiales; Eudicotyledons; Core eudicots;
1 (bases 1 to 549)
REFERENCE 1 Chen, J., Momiyama, M., Chan, E., Mooney, M., Carron, B., Gilliland, D.,
Wang, X., Hillman, J., Guebler, K., Kim, C., Doyle, M., Brzoska, P.,
Gergonne, R., Burns, D., Griffin, J., Mounoudou, M., Nguyen, D.,
Tan, R., Rose, M., Warren, B., Ton, B., Kesteven, K., Borillo, C.,
Carpio, T., Policky, J., Suzuki, G., Argente, C., Shah, S.,
Nobrega, A., Murry, L., Turner, C., Krikorian, S., Elder, L., and
Hansen, D.
TITLE Arabidopsis thaliana Gene Expression Microarray

JOURNAL

Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.
Location/Qualifiers

FEATURES

SOURCE

1. 549
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/cultivar="Columbia Col-0"
/db_xref="taxon:3702"
/clone="701545370"
/issue_type="rosette"
/dev_stage="4 - 7 weeks"
/clone.lib="A. thaliana, Columbia Col-0, rosette-2"
/note="Vector: pSPORT; Site 1: NotI; Site 2: SalI; cDNA
library was derived from untreated rosette tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was initiated
using a NotI-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to SalI adaptors, digested with NotI,
size-selected, and cloned into the NotI and SalI sites of
the pSPORT vector."

ORIGIN

Query Match 29.6%; Score 541.8; DB 9; Length 549;
Best Local Similarity 99.5%; Pred. No. 2.2e-98;
Matches 543; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1270 GGAAGAAAGATCAACCGCTTCTGTTTGTGCTTCTTCTGCAACATTAACCTGATTC 1329
DB 546 GGAAGAAAGATCAACCGCTTCTGTTTGTGCTTCTTCTGCAACATTAACCTGATTC 487
QY 1330 GGGGAGACTTGGCTTGAAGAAAGGAGTACCTCGGATGATTAACAGACGGGAAGT 1389
DB 486 GGGGAGACTTGGCTTGAAGAAAGGAGTACCTCGGATGATTAACAGACGGGAAGT 427
QY 1390 AGAGTTGACACGCTATATGATGATGATGATGATGATGATGATGATGATGATGATG 1449
DB 426 AGAGTTGACACGCTATATGATGATGATGATGATGATGATGATGATGATGATGATG 367
QY 1450 GTTCAATGTTAGACAGTATGCGGTTGAGACCGGTGCAACCGTATACCGTATCTTCT 1509
DB 366 GTTCAATGTTAGACAGTATGCGGTTGAGACCGGTGCAACCGTATACCGTATCTTCT 307
QY 1510 CCGAGCGGCTTATGAGAACCGGGGAATGATGAGCAACCGGATCATGACCGTCACTCAT 1569
DB 306 CCGAGCGGCTTATGAGAACCGGGGAATGATGAGCAACCGGATCATGACCGTCACTCAT 247
QY 1570 GAGGATGAACTTAAAGAGATTAATCGCGGATGCGTAAAGAGATGAGAGCC 1629
DB 246 GAGGATGAACTTAAAGAGATTAATCGCGGATGCGTAAAGAGATGAGAGCC 187
QY 1630 ATTAAATGAATGGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1689
DB 186 ATTAAATGAATGGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 127
QY 1690 AAACAAAATTTAATATTAAGAAATGAGATGATGAGAAATTTCTGCTGCTAATATAT 1749
DB 126 AAACAAAATTTAATATTAAGAAATGAGATGATGAGAAATTTCTGCTGCTAATATAT 67
QY 1750 TTTTTCATGAGGAGCTATGTTTATCATCAATATATCATTTACAAATGATATACCTT 1809
DB 66 TTTTTCATGAGGAGCTATGTTTATCATCAATATATCATTTACAAATGATATACCTT 7
QY 1810 ATCAAT 1815
DB 6 ATCAAT 1

QY	1151	AGAGGGGCTTACATGCTCTGACGAAACGTAAGCTTGGGGAAATTCCTCTGGTTGGAAATGCGCA	121
QY	245	AGAGGGGCTTACATGCTCTGACGAAACGTAAGCTTGGGGAAATTCCTCTGGTTGGAAATGCGCA	304
QY	1211	GTCCACGACACAAATTCAGATATCTCACTCTTGTTACAAATGATTTATGACATTCCTGATG	1270
Db	305	GTCCACGACACAAATTCAGATATCTCACTCTTGTTACAAATGATTTATGACATTCCTGATG	364
QY	1271	GAGAAAGCATCAAAACGGTTCTGTTCCGTTGCTGTCCTGCGAAACATTAACGCTGATTCG	1330
Db	365	GAGAAAGCATCAAAACGGTTCTGTTCCGTTGCTGTCCTGCGAAACATTAACGCTGATTCG	424
QY	1331	-----	1330
Db	425	GGTAAACCATTTAAATCACATGTGTAACCGCGGTTTTTTTAGCGCTTAGTAAAGTAAAT	484
QY	1331	-----GGGACACTTCGCTCGAGAAACCGAGT	1357
Db	445	GGTTTACTTAATTTGTGAAATGTTTTTTGATTTTCAGGAGACCTTGCTCGAGAAACCGAGT	544
QY	1358	GACCTCGGGATCGATMAACAGAACCGGAGATGATGATTTGCAACAGCTATATGATGTCGA	1417
Db	545	GACCTCGGGATCGATMAACAGAACCGGAGATGATGATTTGCAACAGCTATATGATGTCG	604
QY	1418	GATGATTTGCTCTTGGGTTAAAGAGACAGGGTTCAATGTTAGAACTACATGCGCTTT	1477
Db	605	GATGATTTGCTCTTGGGTTAAAGAGACCGGGTTCATGTTAGAACTACATGCGCTTT	664
QY	1478	GGACCCGTGCAACCCGCTATACCGTATCTTCCGACCGCGCTTATGAAACCGGGGAATG	1537
Db	665	GGACCCGTGCAACCGCTATACCGTATCTTCCGACCGCGCTTATGAAACCGGGGAATG	724
QY	1538	ATGGCCACCGGAGCTCATGACC	1559
Db	725	ATGGCCACCGGAGCTCATGACC	746
RESULT 8			
AVS63245/c			
LOCUS	AVS63245	518 bp	mRNA linear EST 07-SEP-2000
DEFINITION	AVS63245 Arabidopsis thaliana green siliques Columbia Arabidopsis		
ACCESSION	AVS63245		
VERSION	AVS63245.1	GI:8734671	
KEYWORDS	EST.		
SOURCE	Arabidopsis thaliana (chale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eutroside II, Brassicales, Brassicaceae, Arabidopsis.		
AUTHORS	1 (bases 1 to 518)		
TITLE	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.		
	A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries		
JOURNAL	DNA Res. 7 (3), 175-180 (2000)		
MEDLINE	20363093		
PUBMED	10907847		
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/. Location/Qualifiers		
FEATURES	1..518		
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	/strain="Columbia"		
	/db_xref="taxon:3702"		
	/clone="SO18304F"		
	/issue_type="green siliques"		
	/clone_lib="Arabidopsis thaliana green siliques Columbia"		

ORIGIN		/note=Vector: plnuescrptii SK; Site_1: EcorI; Site_2: XhoI"
Query Match	28.0%; Score 513; DB 9; Length 518;	
Best Local Similarity	100.0%; Prid. No. 1.6e-92;	
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Dy	1321 CGCTGATTCGGGGAGACTTGTGGTGAGAAACGAGTAGAAGCTCGGGATTCGATTAAACGAA	1380
Dd	518 CGCTGATTCGGGGAGACTTGTGGTGAGAAACGAGTAGAAGCTCGGGATTCGATTAAACGAA	459
Dy	1381 CGGGAAGATAGAGTTTGCAACGACTATAATGTATGTCAATGCATTTGCTTCCGAGTTAAA	1440
Dd	458 CGGGAAGATAGAGTTTGCAACGACTATAATGTATGTCAATGCATTTGCTTCCGAGTTAAA	399
Dy	1441 GAGAGCAGGGTTCAATGTTAGCAAGTACATGCCGTTTGACCCTCGCAACCGCTATACC	1500
Dd	398 GAGAGCAGGGTTCAATGTTAGCAAGTACATGCCGTTTGACCCTCGCAACCGCTATACC	339
Dy	1501 GTATCTTCCGACGCGCTTATGAGAACCGGGGAATATGGCCACCGAGCTCATGACCG	1560
Dd	338 GTATCTTCCGACGCGCTTATGAGAACCGGGGAATATGGCCACCGAGCTCATGACCG	279
Dy	1561 TCAACTCATGAGATGGAATCTTAAGAGAGATTAATGCCGGAGTTGCGTAAAGAGAG	1620
Dd	278 TCAACTCATGAGATGGAATCTTAAGAGAGATTAATGCCGGAGTTGCGTAAAGAGAG	219
Dy	1621 TAGGAGCATTAATGAAATTTGGGAAATGAGATGAAATTAATTTCTTATGATGATTA	1680
Dd	218 TAGGAGCATTAATGAAATTTGGGAAATGAGATGAAATTAATTTCTTATGATGATTA	159
Dy	1681 AGAAATTGAAAAAACAATAATTATATATAAGAAATGAGATGATGAGAACAATTTCTGTG	1740
Dd	158 AGAAATTGAAAAAACAATAATTATATATAAGAAATGAGATGATGAGAACAATTTCTGTG	99
Dy	1741 GCTAAATATTTTCATAGAGACATATTTTTTACTATCAATATATCATTCGAAATGTAT	1800
Dd	98 GCTAAATATTTTCATAGAGACATATTTTTTACTATCAATATATCATTCGAAATGTAT	39
Dy	1801 ATTCACCTTATCATATAAAATGCTTTTACTTT 1833	
Dd	38 ATTCACCTTATCATATAAAATGCTTTTACTTT 6	
RESULT 9		
CD813513	745 bp mRNA linear EST 10-JUL-2003	
LOCUS	BNI5.019002F020121 BNI5 Brassica napus cDNA clone BNI5019002, mRNA	
DEFINITION	sequence.	
ACCESSION	CD813513	
VERSION	CD813513.1 GI:32495453	
KEYWORDS	EST.	
SOURCE	Brassica napus (rape)	
ORGANISM	Brassica napus	
REFERENCE	Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
TITLE	roides; eurosids II; Brassicales; Brassicaceae; Brassica.	
JOURNAL	1 (bases 1 to 745)	
COMMENT	Genopiante. Genopiante, a major partnership french program in plant genomics Unpublished (2003) Contact: Genopiante Genopiante 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10 This sequence has been generated in the framework of the french plant genomics programme 'Genopiante' (http://www.genopiante.com and http://genopiante-info.infobiogen.fr). Location/Qualifiers 1..745 /organism="Brassica napus"	
FEATURES		
SOURCE		

Db 483 AAGGAGTACCTCGGAGTGAATTAACAGACGGAGATGAGTTGCAACGCTATAT 424
 QY 1409 GGTATGTCAGATGATGCTTCTCGGTTAAAGAGAGAGGCTTCAATGTTAGCAAGTAC 1468
 Db 423 GGTATGTCAGATGATGCTTCTCGGTTAAAGAGAGAGGCTTCAATGTTAGCAAGTAC 364
 QY 1469 ATGCGTTTGAACCCGTCGCAACCGCTATACCGTATCTTCTCGAGCGCTTATGAGAAC 1528
 Db 363 ATGCGTTTGAACCCGTCGCAACCGCTATACCGTATCTTCTCGAGCGCTTATGAGAAC 304
 QY 1529 CGGGAGATGATGGCCAGCGAGCTCATGACCGTCACTCATGAGAGATGAGAACTTAAAGG 1588
 Db 303 CGGGAGATGATGGCCAGCGAGCTCATGACCGTCACTCATGAGAGATGAGAACTTAAAGG 244
 QY 1589 AGATTATTCGCGGAGATTCGCTAAAGAGAGATGAGAGCCATTAATGAAATGGAGAA 1648
 Db 243 AGATTATTCGCGGAGATTCGCTAAAGAGAGATGAGAGCCATTAATGAAATGGAGAA 184
 QY 1649 TGTGATGATTAATTTCTTCTATGATGTTAAAGAAATGAAAAAATTTATATAT 1708
 Db 183 TGTGATGATTAATTTCTTCTATGATGTTAAAGAAATGAAAAAATTTATATAT 124
 QY 1709 AAGAAATGAGTAAAGAGATTCCTGCTAAATATTTTTCATGAGGAGCTATGT 1768
 Db 123 AAGAAATGAGTAAAGAGATTCCTGCTAAATATTTTTCATGAGGAGCTATGT 64
 QY 1769 TTTTACTCTCAATATATCATTCACAAATGATATTCACCTTATCAATTAATGCTTTT 1828
 Db 63 TTTTACTCTCAATATATCATTCACAAATGATATTCACCTTATCAATTAATGCTTTT 4
 QY 1829 ACT 1831
 Db 3 CCT 1

RESULT 13
 CD813554 720 bp mRNA linear EST 10-JUL-2003
 LOCUS BN15.020B05F020211 BN15 Brassica napus cDNA clone BN15020B05, mRNA
 DEFINITION
 ACCESSION CD813554
 VERSION CD813554.1 GI:32495494
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 720)
 AUTHORS Genopiante.
 TITLE Unpublished, a major partnership french program in plant genomics
 JOURNAL Contact: Genopiante
 COMMENT
 Genopiante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genopiante' (<http://www.genopiante.com>
 and <http://genopiante-info.inbio.gen.fr>).
 Location/Qualifiers
 1..720
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cullivar="Uet neuf"
 /db_xref="taxon:3708"
 /clone="BN15020B05"
 /tissue_type="seed"
 /clone_id="BN15"

ORIGIN
 Query Match 25.9%; Score 475.4; DB 14; Length 720;
 Best Local Similarity 82.4%; Pred. No. 4.9e-85;

Matches 573; Conservative 0; Mismatches 111; Indels 11; Gaps 2;
 QY 8 AGAAAAAACACCGATTAACCGAAACATCAAGCAACAAAAAAGAGAGAAAT 67
 Db 37 AGAGAAAAAGCGAATAATCCGAAAGCTTAAGAAACATCAAAAGAGATTAACAT 96
 QY 68 TATTTTTTTTTTTGTTTTGTTTTCAAAAAAATAATCTTTGAATTTTATGCAACCCGCTT 127
 Db 97 TTTCTTTTTTTG-----TTTCAAAAGGAAATCTTTGAATTTTATGCAACCCGCTT 148
 QY 128 CTCGAAACAACTTTATTCGGGATCTTACCGTTTAAACCGCTTTTAAACCGGTTGGTCT 187
 Db 149 CTCGAAACAACTTTATTCGGGATCTTACCGTTTAAACCGGTTGGTCTCA 208
 QY 188 CCCACCGTACTGCTTCCACCGCGTGTCCGAGATCTCTCTGTTGAACAAGCA 247
 Db 209 CCCACCGTAAACGCTTCAACAGCCGCGGATTTCTCTCTGTTGAACAAGCA 268
 QY 248 CCGGAAACCACTCTTCAACCAACCAACCAACCAACCAATCTCAAGATGCTCATCTC 307
 Db 269 CCGAGCCCACTCTCAACCAACCAACCAACCAACCAACCAATCTCAAGATGCTCATCTC 325
 QY 308 TCGATCAAGCCCGTCTTCTCTCTCTATCCCAACCTGATCTCTCGCTCCACCGCC 367
 Db 326 TCGACCAAGCCCGTCTCTCTCTCTATCCCAACCTGATCTCTCGCTCCACCGCC 385
 QY 368 GTGTGATGATGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 427
 Db 386 GTGTGATGATGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 445
 QY 428 AATCTTATGAGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
 Db 446 AATCTTATGAGAGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 505
 QY 488 TATGACATTTTGGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
 Db 506 TATGACATTTTGGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
 QY 548 TATGAGACTACTGCTTAAAGAGATGCTTGTATGAGCTGTAACACCGGATGATGAT 607
 Db 566 TATGAGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 625
 QY 608 GTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
 Db 626 GCCACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 685
 QY 668 CCAACATCTCACTTATGCTCAAGTGTGTAAGAT 702
 Db 686 CCAACATCTCACTTATGCTCAAGTGTGTAAGAT 720

RESULT 14
 CD835442 713 bp mRNA linear EST 10-JUL-2003
 LOCUS BN45.045I07F011229 BN45 Brassica napus cDNA clone BN45045I07, mRNA
 DEFINITION
 ACCESSION CD835442
 VERSION CD835442.1 GI:32517382
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 713)
 AUTHORS Genopiante.
 TITLE Unpublished, a major partnership french program in plant genomics
 JOURNAL Contact: Genopiante
 COMMENT
 Genopiante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES

Source

1. 713
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jec neuf"
/db_xref="taxon:3708"
/clone="BN45045107"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN

Query Match 25.3%; Score 463; DB 14; Length 713;
Best Local Similarity 80.9%; Pred. No. 1.5e-82;

Matches 564; Conservative 0; Mismatches 130; Indels 4; Gaps 2;

11 AAAAAACAGCATTAACCGAAACATCAAGCAAAACAAAAAGAGAGAAATAT 70
19 AG 78

71 TTTTGTGTTTGTGTTTCAAAACAAATCTTGAATTTATGCAACCGCTCTTC 130
79 ACAATTTTATTTTGTGTTTATCAAGACATCTTGAATTTATGCAACCGCTCTTC 138

131 CGAGCAAACTTTATCCGGGAGATCTTACCGTTTACCGCTTTAGCCCGGTCTCTCC 190
139 CGAGCAAACTTTATCCGGGAGATCTTACCGTTTACCGCTTTAGCCCGGTCTCTCC 198

191 ACCGTACTGCTTCAACCGCGCTCTCCGAGATCTCTCTTGAACAACAACGCG 250
199 ACCGTACTGCTTCAACCGCGCTCTCCGAGATCTCTCTTGAACAACAACGCG 258

251 GAACCACTCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 310
259 GAACCACTCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 315

311 GATCAAGCCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 370
316 GATCAAGCCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 375

371 TTGATGCGCGCGAGTAGGTCTTATGATGATGATGATGATGATGATGATGAT 430
376 TTGATGCGCGCGAGTAGGTCTTATGATGATGATGATGATGATGATGATGAT 435

431 CTATGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 490
436 CTATGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 495

491 GACATTTTGGCGCGGTGAAGATGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 550
496 GACATTTTGGCGCGGTGAAGATGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 555

551 GAAGCTACTGCTTTAAAGGATGCTTGTCTATGCGGTGAAGACGCGGATGCT 610
556 GAAGCTACTGCTTTAAAGGATGCTTGTCTATGCGGTGAAGACGCGGATGCT 615

611 TCTTGATGATTAACATGCAACATCATTCGACATGAAGCTGCAAACTTTACCA 670
616 TCTTGATGATTAACATGCAACATCATTCGACATGAAGCTGCAAACTTTACCA 675

671 ACATCTCACTTATAGTCAAGTGTGTGAAGATTAAGTGC 708
676 ACATCTCACTTATAGTCAAGTGTGTGAAGATTAAGTGC 712

RESULT 15
CD825384 698 bp mRNA linear EST 10-JUL-2003

LOCUS BN25.060J17F011129 BN25 Brassica napus cDNA clone BN25060J17, mRNA

DEFINITION sequence.

ACCESSION CD825384

VERSION CD825384.1 GI:32507324
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 698)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante.
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante

FEATURES

Source

93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

1. 698
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jec neuf"
/db_xref="taxon:3708"
/clone="BN25060J17"
/tissue_type="seed"
/clone_lib="BN25"

ORIGIN

Query Match 24.9%; Score 456.4; DB 14; Length 698;
Best Local Similarity 80.9%; Pred. No. 3.2e-81;

Matches 545; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

11 AAAAAACAGCATTAACCGAAACATCAAGCAAAACAAAAAGAGAGAAATAT 70
28 AG 87

71 TTTTGTGTTTGTGTTTCAAAACAAATCTTGAATTTATGCAACCGCTCTTC 130
88 ACAATTTTATTTTGTGTTTATCAAGACATCTTGAATTTATGCAACCGCTCTTC 147

131 CGAGCAAACTTTATCCGGGAGATCTTACCGTTTACCGCTTTAGCCCGGTCTCTCC 190
148 CGAGCAAACTTTATCCGGGAGATCTTACCGTTTACCGCTTTAGCCCGGTCTCTCC 207

191 ACCGTACTGCTTCAACCGCGCTCTCCGAGATCTCTCTTGAACAACAACGCG 250
208 ACCGTACTGCTTCAACCGCGCTCTCCGAGATCTCTCTTGAACAACAACGCG 267

251 GAACCACTCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 310
268 GAACCACTCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 324

311 GATCAAGCCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 370
325 GATCAAGCCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 384

371 TTGATGCGCGCGAGTAGGTCTTATGATGATGATGATGATGATGATGATGAT 430
385 TTGATGCGCGCGAGTAGGTCTTATGATGATGATGATGATGATGATGATGAT 444

431 CTATGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 490
445 CTATGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 504

491 GACATTTTGGCGCGGTGAAGATGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 550
505 GACATTTTGGCGCGGTGAAGATGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 564

551 GAAGCTACTGCTTTAAAGGATGCTTGTCTATGCGGTGAAGACGCGGATGCT 610
565 GAAGCTACTGCTTTAAAGGATGCTTGTCTATGCGGTGAAGACGCGGATGCT 624

Qy 611 TCTTGATGATACATGCAACATTCATTGGAACCATGGAAGCTGCCAAATCTTTACCA 670
Db 625 TCTTGATGATACATGCAACATTCATTGGAACCATGGAAGCTGCCAAATCTTTACCA 684
Qy 671 ACATCTCACTTTAG 684
Db 685 ACATCTCACTTTAG 698

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